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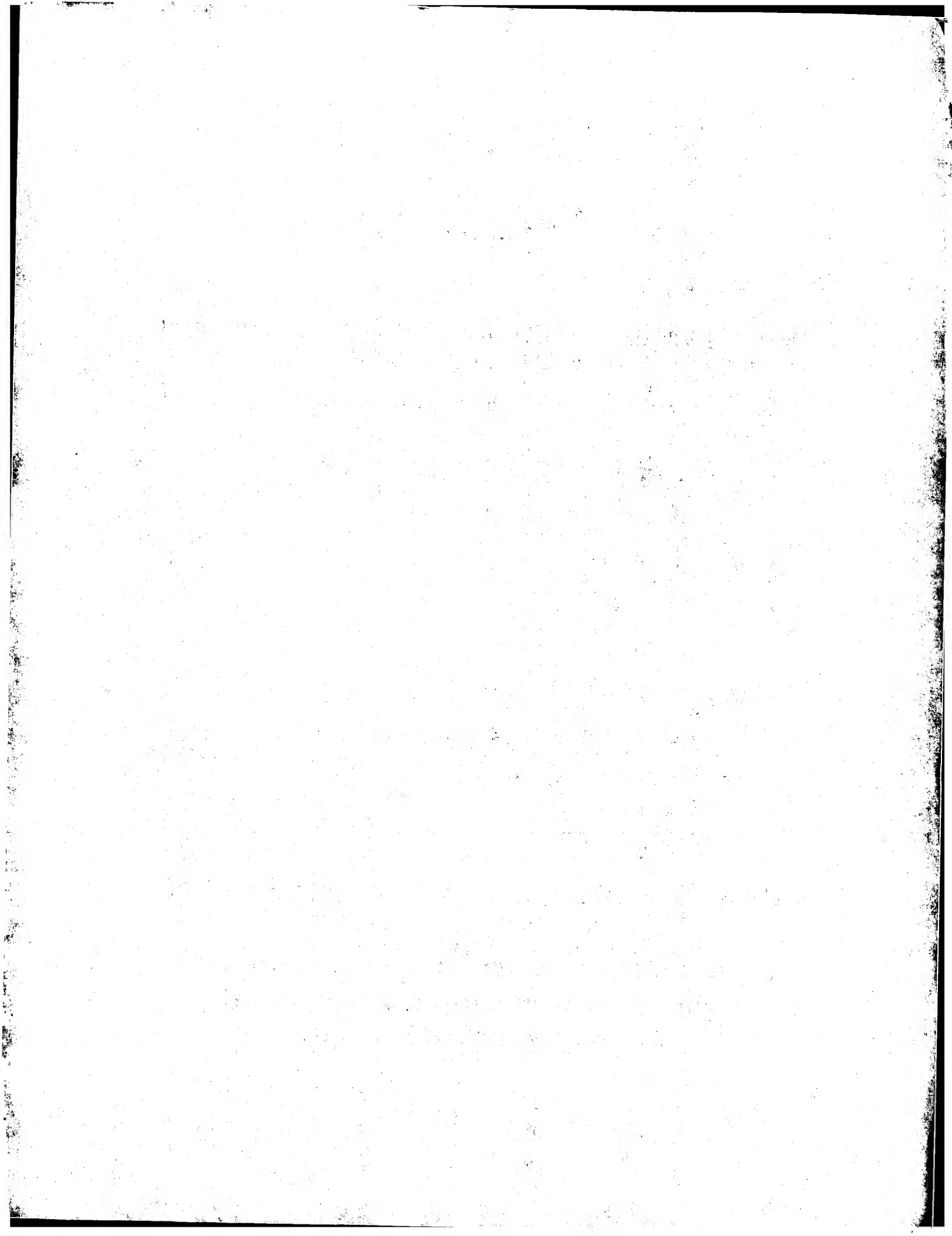
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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER (57) Abstract Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.		

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COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD

The present invention relates generally to the detection and therapy of breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. See, e.g., Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in

breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated DNA molecules are provided, comprising (a) a nucleotide sequence preferentially expressed in breast cancer tissue, relative to normal tissue; (b) a variant of such a sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% (preferably no more than 5%) of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one of the above sequences. In one embodiment, the isolated DNA molecule comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated DNA molecule comprises a nucleotide sequence recited in any one of SEQ ID NO: 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

In related embodiments, the isolated DNA molecule encodes an epitope of a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219,

221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297; and wherein RNA corresponding to said nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue.

5 In another embodiment, the present invention provides an isolated DNA molecule encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide
10 positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a DNA molecule as described above are also provided.

 In related aspects, the present invention provides recombinant expression
15 vectors comprising a DNA molecule as described above and host cells transformed or transfected with such expression vectors.

 In further aspects, polypeptides, comprising an amino acid sequence encoded by a DNA molecule as described above, and monoclonal antibodies that bind to such polypeptides are provided.

20 In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method
25 comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described ,
above wherein the polypeptide is encoded by a nucleotide sequence selected from the
30 group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208,

215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more
5 monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

10 Within a related aspect, the diagnostic kit comprises a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for an RNA molecule described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of an RNA molecule as described above, or an RNA molecule encoding a polypeptide encoded by a
15 nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a DNA molecule described herein.
20 In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a DNA molecule as described above, or a DNA molecule selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

25 In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and
30 therefrom monitoring the progression of breast cancer in the patient. In another

embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA molecule encoding a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immune response enhancer or adjuvant, are provided. In yet other aspects, the present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2)

and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

5 Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

Figure 4 is a genomic clone map showing the location of additional retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID
10 NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

15 Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

Figure 9 shows the nucleotide sequence of the representative breast
20 tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

25 Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

Figure 14 shows the nucleotide sequence of the representative breast
30 tumor-specific cDNA B9CG1.

Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

5 Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

10 Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA1.

Figure 21A depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

15 Figure 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 20 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer.

25 The compositions described herein include polypeptides, nucleic acid sequences and antibodies. Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (*i.e.*, the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-

specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Nucleic acid sequences of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence.

5 Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

10 Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retroviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141).

15 Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 - SEQ ID NO:10. B18Ag1 has homology to the *gag* p30 gene of the endogenous human retroviral element S71, as described in Werner et al., *Virology* 174:225-238 (1990) and also shows homology to about thirty other retroviral *gag* genes. As discussed in more detail below, the present invention also includes a number of additional breast tumor-
20 specific polypeptides, such as those encoded by the nucleotide sequences recited in SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including
25 full length proteins containing the sequences recited herein. A polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may (but, need not) possess immunogenic or antigenic properties.

An "epitope," as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

The compositions and methods of the present invention also encompass variants of the above polypeptides and nucleic acid sequences encoding such polypeptides. A polypeptide "variant," as used herein, is a polypeptide that differs from the native polypeptide in substitutions and/or modifications, such that the antigenic and/or immunogenic properties of the polypeptide are retained. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antisera and/or T-cells as described above. Nucleic acid variants may contain one or more substitutions, deletions, insertions and/or modifications such that the antigenic and/or immunogenic properties of the encoded polypeptide are retained. One preferred variant of the polypeptides described herein is a variant that contains nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another

amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr;
5 (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenic or antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For
10 example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a
15 polypeptide may be conjugated to an immunoglobulin Fc region.

In general, nucleotide sequences encoding all or a portion of the polypeptides described herein may be prepared using any of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential
20 display PCR. This technique compares the amplified products from RNA template prepared from normal and breast tumor tissue. cDNA may be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and subcloned into a suitable
25 vector (e.g., the T-vector, Novagen, Madison, WI). Nucleotide sequences encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID NO.:87-125.

Alternatively, a gene encoding a polypeptide as described herein (or a
30 portion thereof) may be amplified from human genomic DNA, or from breast tumor

cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and
5 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). An amplified portion of B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within
10 the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral
15 promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11 - SEQ ID NO:86 and SEQ ID
20 NO:142 - SEQ ID NO:297.

Recombinant polypeptides encoded by the DNA sequences described above may be readily prepared from the DNA sequences. For example, supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter.
25 Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this
30 invention. Expression may be achieved in any appropriate host cell that has been

transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

5 Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other
10 variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing
15 amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division,, Foster City, CA, and may be operated according to the manufacturer's instructions.

 In specific embodiments, polypeptides of the present invention
20 encompass amino acid sequences encoded by a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297, variants of such polypeptides that are encoded by DNA molecules containing
25 one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, and epitopes of the above polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-
30 166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240,

243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. DNA molecules according to the present invention include molecules that encode any of the above polypeptides.

In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519 (1976), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as

described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and
5 then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having
10 high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from
15 the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast
20 cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

25 There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis,
30 transferred to a suitable membrane and allowed to react with the antibody. The

presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of

antibody ranging from about 10 ng to about 1 μ g, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.,* incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least, 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium

may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support
5 with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard
10 methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed
15 and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different
20 reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of breast cancer, the signal
25 detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor tissue. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients, without breast cancer. In general, a sample generating a signal that is three standard
30 deviations above the predetermined cut-off value may be considered positive for breast

cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, p. 106-7 (Little Brown and Co., 1985). Briefly, in this embodiment, the cut-off value may be determined from a plot of
5 pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered
10 positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or
15 strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody
20 may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the
25 concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that, would be sufficient to generate a positive signal in the two-antibody sandwich assay, in
30 the format discussed above. Preferably, the amount of antibody immobilized on the

membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μ g. Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be
5 determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (e.g., a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an evaluation may be achieved using any of a variety of methods known to those of ordinary skill in the art such as, for example, *in situ* hybridization and
10 amplification by polymerase chain reaction.

For example, polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above biological samples. Sequence-specific primers for use in such amplification may be designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86 and 142-
15 297, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art.
20 Amplification is typically performed on samples obtained from matched pairs of tissue (tumor and non-tumor tissue from the same individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the
25 tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a DNA/RNA molecule" means an oligonucleotide sequence that has at least about 80% identity preferably at least about 90% and more preferably at least about 95%, identity to the
30 DNA/RNA molecule in question. Primers and/or probes which may be usefully

employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers comprise at least about 10 contiguous nucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in
5 the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide
10 staining while important in defining gene specificity do not lend themselves to diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can
15 be modified for use in 96 well plate formats. Instrumentation to perform such methodologies are available from Perkin Elmer/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxigenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

20 In yet another method for determining the presence or absence of breast cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more
25 polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater
30 in patients that have been exposed previously to a test antigen (*i.e.*, an immunogenic

portion of a polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

5 The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to 100 μ g, preferably from about 10 μ g to 50 μ g
10 in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80™.

 In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays
15 over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast,
20 breast cancer is not progressing when the signal detected either remains constant or decreases with time.

 In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the compounds (which may be polypeptides, antibodies or nucleic acid molecules) are
25 preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more polypeptides and an immune response enhancer, such as an adjuvant or a liposome (into which the compound is incorporated). Pharmaceutical compositions and vaccines may additionally contain a delivery system,
30 such as biodegradable microspheres which are disclosed, for example, in U.S. Patent

Nos. 4,897,268 and 5,075,109. Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, including one or more separate polypeptides.

Alternatively, a vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749 (1993), and reviewed by Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention.

Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. To prevent the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a patient with breast cancer, the pharmaceutical composition or vaccine may comprise one or more polypeptides, antibodies or nucleotide sequences complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients.

A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*.

- 5 Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about
- 10 100 μ g to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC cDNAs USING DIFFERENTIAL DISPLAY RT-PCR

This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO.:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (CTTCAACCTC) (SEQ ID NO.:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products was obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus, (SSV). S71 contains an incomplete *gag* gene, a portion of the *pol* gene and an LTR-like structure at the 3' terminus (*see* Werner et al., *Virology* 174:225-238 (1990)). B18Ag1

is also 64% identical to SSV in the region corresponding to the P30 (gag) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of gag proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the gag gene, but
5 spans several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C → 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence present at relatively high levels in the patient's breast tumor tissue. The primers used
10 in amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO.:128) and B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO.:129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127) at 2 mM magnesium at pH 9.5. The same
15 experiments showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (see Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the
20 B18Ag1 transcript is not present in various normal tissues (including lymph node, myocardium and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also
25 confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents
30 normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin,

lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be present in human genomic DNA as a single copy endogenous retroviral element. A genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion. Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the location of the sequence labeled 3, SEQ ID NO:6 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 14 and SEQ ID NO:10 shows the location of the sequence labeled 11-22.

Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic clone. The box below this line shows the position of selected restriction sites. The arrows depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within the element. The open boxes correspond to predicted reading frames, starting with a

methionine, found throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was
5 obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%) compared to the genomic sequence shown in SEQ ID NO:141.

B. Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides

Normal RNA and tumor RNA was prepared and mRNA was isolated and
10 converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above. Differential display PCR was then executed using the randomly chosen primers SEQ ID NO.: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into either the T-vector (Novagen, Madison, WI) or the pCRII vector
15 (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO.:11-26 and 28-77) (*see also* Figures 6-20).

An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in
20 further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene bank as described above, revealed homology to the known human β -A activin gene.

Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-
25 240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In further studies, six different splice forms of the antigen B11Ag1 were
30 isolated, with each of the various splice forms containing slightly different versions of

the B11Ag1 coding frame. Splice junction sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the original B11Ag1 clone, with expression being breast tumor, prostate and testis-specific. The determined cDNA sequences for the isolated protein coding exons are provided in SEQ ID NO: 292-297, respectively.

EXAMPLE 2

10 PREPARATION OF B18AG1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA using 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

25 EXAMPLE 3

PREPARATION OF B18AG1 DNA FROM BREAST TUMOR cDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μ l. After first strand synthesis, the cDNA is diluted approximately 25 fold and 1 μ l is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18Ag1

This Example illustrates the identification of B18Ag1 epitopes.

The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for hydrophobicity and hydrophilicity values using the method of Hopp, *Prog. Clin. Biol. Res.* 172B:367-77 (1985) or, alternatively, Cease et al., *J. Exp. Med.* 164:1779-84 (1986) or Spouge et al., *J. Immunol.* 138:204-12 (1987). Additional Class II MHC (antibody or B-cell) epitopes can be predicted using programs such as AMPHI (*e.g.*, Margalit et al., *J. Immunol.* 138:2213 (1987)) or the methods of Rothbard and Taylor (*e.g.*, *EMBO J.* 7:93 (1988)).

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems Division, Foster City, CA) and techniques such as Merrifield synthesis. Following synthesis, the peptides can be used to screen sera harvested from either normal or breast cancer patients to determine whether patients with breast cancer possess antibodies

reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can also be tested for their ability to generate a serologic or humoral immune in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC molecules. (*see, e.g., Rammensee et al., Immunogenetics 41:178-228 (1995)*). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (*e.g., Sette et al., J. Immunol. 153:5586-92 (1994)*) and more importantly can be tested for their ability to generate antigen reactive cytotoxic T-cells following *in vitro* stimulation of patient or normal peripheral mononuclear cells using, for example, the methods of Bakker et al., *Cancer Res. 55:5330-34 (1995)*; Visseren et al., *J. Immunol. 154:3991-98 (1995)*; Kawakami et al., *J. Immunol. 154:3961-68 (1995)*; and Kast et al., *J. Immunol. 152:3904-12 (1994)*. Successful *in vitro* generation of T-cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following *in vitro* peptide stimulation further confirms the immunogenicity of the B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following *in vivo* immunization in mice rendered transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., *J. Exp. Med. 173:1007-15 (1991)*).

A representative list of predicted B18Ag1 B-cell and T-cell epitopes, broken down according to predicted HLA Class I MHC binding antigen, is shown below:

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI

QGAAQKPINLSKXIEVVQGHDE

SPGVFLEHLQEAYRIYTPFDLSA

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

YLLVGIQGA
5 GAAQKPINL
NLSKXIEVV
EVVQGHDES
HLQEAYRIY
NLAQVAQAA
10 FVAQAAPDS

EXAMPLE 5

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

15

The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in
20 a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

To ensure the semiquantitative nature of the RT-PCR, β -actin was used
25 as internal control for each of the tissues examined. Serial dilutions of the first strand cDNAs were prepared and RT-PCR assays performed using β -actin specific primers. A dilution was then selected that enabled the linear range amplification of β -actin template, and which was sensitive enough to reflect the difference in the initial copy number. Using this condition, the β -actin levels were determined for each reverse
30 transcription reaction from each tissue. DNA contamination was minimized by DNase

treatment and by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

15	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
20	Other Tissues	Over-expressed in Breast Tumors but <u>not in any Normal Tissues</u>	9%
		Over-expressed in Breast Tumors but Expressed in Some Normal Tissues	30%
25		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
- (iii) NUMBER OF SEQUENCES: 297
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 04-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.419C2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTA GAG ACC CAA TTG GGA CCT AAT TGG GAC CCA AAT TTC TCA AGT GGA	48
Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
GGG AGA ACT TTT GAC GAT TTC CAC CGG TAT CTC CTC GTG GGT ATT CAG	96
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
GGA GCT GCC CAG AAA CCT ATA AAC TTG TCT AAG GCG ATT GAA GTC GTC	144
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
CAG GGG CAT GAT GAG TCA CCA GGA GTG TTT TTA GAG CAC CTC CAG GAG	192
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
GCT TAT CGG ATT TAC ACC CCT TTT GAC CTG GCA GCC CCC GAA AAT AGC	240
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
CAT GCT CTT AAT TTG GCA TTT GTG GCT CAG GCA GCC CCA GAT AGT AAA	288
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
AGG AAA CTC CAA AAA CTA GAG GGA TTT TGC TGG AAT GAA TAC CAG TCA	336
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
100 105 110	
GCT TTT AGA GAT AGC CTA AAA GGT TTT	363
Ala Phe Arg Asp Ser Leu Lys Gly Phe	
115 120	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	

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65              70              75              80
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys
              85              90              95
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser
              100              105              110
Ala Phe Arg Asp Ser Leu Lys Gly Phe
              115              120

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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TCTTAGAATC TTCATACCCC GAACTCTTGG GAAAACCTTTA ATCAGTCACC TACAGTCTAC      60
CACCCATTTA GGAGGAGCAA AGCTACCTCA GTCCTCCGG AGCCGTTTTA AGATCCCCCA      120
TCTTCAAAGC CTAACAGATC AAGCAGCTCT CCGGTGCACA ACCTGCGCCC AGGTAAATGC      180
CAAAAAAGGT CCTAAACCCA GCCCAGGCCA CCGTCTCCAA GAAAACTCAC CAGGAGAAAA      240
GTGGGAAATT GACTTTACAG AAGTAAAACC ACACCGGGCT GGGTACAAAT ACCTTCTAGT      300
ACTGGTAGAC ACCTTCTCTG GATGGACTGA AGCATTGCT ACCAAAAACG AAAGTGTCAA      360
TATGGTAGTT AAGTTTTTAC TCAATGAAAT CATCCCTCGA CGTGGGCTGC CTGTTGCCAT      420
AGGGTCTGAT AATGGAACGG CCTTCGCCTT GTCTATAGTT TAATCAGTCA GTAAGGCGTT      480
AAACATTCAA TGGAAGCTCC ATTGTGCCTA TCGACCCAGA GCTCTGGGCA AGTAGAACGC      540
ATGAACTGCA CCCTAAAAAA ACACTCTTAC AAAATTAATC TTAAAAACCG GTGTTAATTG      600
TGTTAGTCTC CTTCCTTAG CCCTACTTAG AGTTAAGGTG CACCCCTTAC TGGGCTGGGT      660
TCTTTACCTT TTGAAATCAT NTTTNGGAAG GGGCTGCCTA TCTTTNCTTA ACTAAAAAAN      720
GCCCATTTGG CAAAAATTC NCAACTAATT TNTACGTNCC TACGTCTCCC CAACAGGTAN      780
AAAAATCTNC TGCCCTTTTC AAGGAACCAT CCCATCCATT CCTNAACAAA AGGCCTGCCN      840
TTCTTCCCCC AGTTAACTNT TTTTNTTAA AATTCCCAA AAANGAACCN CCTGCTGGAA      900
AAACNCCCCC CTCCAANCCC CGGCCNAAGN GGAAGTTCC CTTGAATCCC NCCCCNCNA      960
ANGGCCCGGA ACCNTTAAAN TNGTTCCNGG GGGTNNGGCC TAAAAGNCCN ATTTGGTAAA     1020
CCTANAAATT TTTTCTTTN TAAAAACCAC NNTTTNNTTT TTCTTAAACA AAACCCTNTT     1080
TNTAGNANCN TATTCCCNC C                                     1101

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TCTAGAGCTG CGCCTGGATC CCGCCACAGT GAGGAGACCT GAAGACCAGA GAAAACACAG      60
CAAGTAGGCC CTTTAAACTA CTCACCTGTG TTGTCTTCTA ATTTATTCTG TTTTATTTTG      120
TTTCCATCAT TTAAAGGGGT TAAATCATC TTGTTCAGAC CTCAGCATAT AAAATGACCC      180
ATCTGTAGAC CTCAGGCTCC AACCATACCC CAAGAGTTGT CTGGTTTTGT TTAAATTACT      240
GCCAGGTTTC AGCTGCAGAT ATCCCTGGAA GGAATATTCC AGATTCCCTG AGTAGTTTC      300

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AGGTTAAAAT	CCTATAGGCT	TCTTCTGTTT	TGAGGAAGAG	TTCCTGTCAG	AGAAAAACAT	360
GATTTTGGAT	TTTTAACTTT	AATGCTTGTG	AAACGCTATA	AAAAAAATTT	TCTACCCCTA	420
GCTTTAAAGT	ACTGTTAGTG	AGAAATTAAA	ATTCCTTCAG	GAGGATTAAA	CTGCCATTTC	480
AGTTACCCTA	ATTCCAAATG	TTTTGGTGGT	TAGAATCTTC	TTAATGTTC	TTGAAGAAGT	540
GTTTTATATT	TTCCCATCNA	GATAAATTCT	CTCNCNCCTT	NNTTTTNTNT	CTNNTTTTTT	600
AAAACGGANT	CTTGCTCCGT	TGTCCANGCT	GGGAATTTTN	TTTTGGCCAA	TCTCCGCTNC	660
CTTGCAANAA	TNCTGCNTCC	CAAAATTACC	NCCTTTTTCC	CACCTCCACC	CCNNGGAATT	720
ACCTGGAATT	ANAGGCCCCC	NCCCCCCCCC	CGGCTAATTT	GTTTTTGTTT	TTAGTAAAAA	780
ACGGGTTTTCC	TGTTTTAGTT	AGGATGGCCC	ANNTCTGACC	CCNTNATCNT	CCCCCTCNGC	840
CCTCNAATNT	TNGGNNTANG	GCTTACCCCC	CCCNNGNNGT	TTTCCTCCAT	TNAAATTTTC	900
TNTGGANTCT	TGAATNNCGG	GTTTTCCCTT	TAAACCENAT	TTTTTTTTTN	NNNCCCCCAN	960
TTTTNCCTCC	CCCNTNTNTA	ANGGGGGTTT	CCCAANCCGG	GTCCNCCCCC	ANGTCCCCAA	1020
TTTTTCTCCC	CCCCCTCTT	TTTTCTTTNC	CCCAAAANTC	CTATCTTTTC	CTNNAAATAT	1080
CNANTNT						1087

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACCAA	GAAATGGGAG	GATTTTAGAG	TGACTGATGA	TTTCTCTATC	ATCTGCAGTT	60
AGTAAACATT	CTCCACAGTT	TATGCAAAAA	GTAACAAAAC	CACTGCAGAT	GACAAACACT	120
AGGTAACACA	CATACTATCT	CCCAAATACC	TACCCACAAG	CTCAACAATT	TTAAACTGTT	180
AGGATCACTG	GCTCTAATCA	CCATGACATG	AGGTCACCAC	CAAACCATCA	AGCGCTAAAC	240
AGACAGAATG	TTTCCACTCC	TGATCCACTG	TGTGGGAAGA	AGCACCGAAC	TTACCCACTG	300
GGGGGCGCTG	NTCANAAANAA	AAGCCCATGC	CCCCGGGTNT	NCCTTTNAAC	CGGAACGAAT	360
NAACCCACCA	TCCCCACANC	TCCTCTGTTC	NTGGGCGCTG	CATCTTGTGG	CCTCNTNTNC	420
TTTNGGGGAN	ACNTGGGGAA	GGTACCCCAT	TTCNTTGACC	CCNCNANAAA	ACCCNGTG	480
CCCTTTGCC	TGATTNCNT	GGGCCTTTTC	TCTTTTCCCT	TTTGGGTTGT	TTAAATTCCC	540
AATGTCCCN	GAACCTCTC	CNTNCTGCCC	AAAACCTACC	TAAATTNCTC	NCTANGNNTT	600
TTCTTGGTGT	TNCTTTTCAA	AGGTNACCTT	NCCTGTTCAN	NCCCNACNAA	AATTTNTTCC	660
NTATNNTGNN	CCCNAAAAA	NNNATCNACC	CNAATTGCCC	GAATTGGTTN	GGTTTTTCCT	720
NCTGGGGGAA	ACCTTTTAAA	TTTCCCCCTT	GGCCGGCCCC	CCTTTTTTCC	CCCCTTTNGA	780
AGGCAGGNGG	TTCTTCCCGA	ACTTCCAATT	NCAACAGCCN	TGCCCCATTG	TGAAACCCTT	840
TTCTAGAAAT	TAAAAAATAN	CCGTTTNNGG	NNGGCCTCTT	TCCCCCTCNG	GNGGGNNGNG	900
AAANTCCTTA	CCCCNAAAAA	GGTTGCTTAG	CCCCCNGTCC	CCACTCCCCC	NGGAAAAATN	960
AACCTTTTCN	AAAAAAGGAA	TATAANTTTN	CCACTCCTTN	GTTCTCTTCC		1010

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGAGCTC	GCGGCCGCGA	GCTCTAATAC	GACTCACTAT	AGGGCGTCGA	CTCGATCTCA	60
GCTCACTGCA	ATCTCTGCCC	CCGGGGTCAT	GCGATTCTCC	TGCCTCAGCC	TTCCAAGTAG	120
CTGGGATTAC	AGGCGTGCAA	CACCACACCC	GGCTAATTTT	GTATTTTAA	TAGAGATGGG	180
GTTTCCCTT	GTTGGCCANN	ATGGTCTCNA	ACCCCTGACC	TCNNGTGATC	CCCCNCCCN	240
NGANCTCNA	CTGCTGGGGA	TNNCCGNMNN	NNCCTCCCN	NCNCNNNNNN	NCNCNNTCCN	300
TNNTCCTTNC	TCNNNNNNNN	CNNTCNNTCC	MNCTTCTCNC	CNNNTNTTNT	CNNCNNCCNN	360
CNNCCNCNT	NCCNCNNNT	TCNCNTNCNN	TNTCCNNCNC	NNTCNNCNNN	CNNNNCNTNN	420
CCNNTACNTC	NTNNNCNNNT	CCNTCTNTNN	CCTCNNCNCN	CNCTNCNCNT	TNTCTCCTCN	480
NTNNNNNNCT	CCNNNNNTCT	CNTCNCNNCN	TNCCTCNCNTN	NCCNCNCCCC	NCCTCNCNNC	540
CTNNTTTNNN	CNNCNCNTCC	NTNCCNTTCN	NNTCCNNTNN	CNNCNTCNCN	NNCNTTNTTC	600
CCNCCNNTTC	CTTNCNCNTN	NNNTNTCNCN	CNCNTCNCNT	NTTNTCTCCT	NNNTCCCNCN	660
TCNNTTCNCC	CNNNTCCNCC	CCCCNCCTNT	CTCTCNCNCN	NNTNNTNTN	NNNCNTCCNC	720
TNTCNCNTTC	NTCNCNTCNC	TNCTNTCNCN	NNCNCNTCNC	TNCCNTNTNT	CTNNNTCNCN	780
TCNCNTNTCN	CCNTCCNTTN	CTNTCTCCTN	TNTCCTTCCC	CTCNCCTNCT	CNTTCNCCNC	840
CCNNTNTNTN	TNNCNCNCNT	NCTNNCNCNC	CNTCNTTTCN	TCTCTNCTNN	NNNTNCCCTC	900
NNCCNTNCC	CTNNTNCNCT	NCTNNTACCN	TNCTNCTCCN	TCTTCTTCC		950

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTAGAGCTC	GCGGCCGCGA	GCTCAATTAA	CCCTCACTAA	AGGGAGTCGA	CTCGATCAGA	60
CTGTTACTGT	GTCTATGTAG	AAAGAAGTAG	ACATAAGAGA	TTCCATTTTG	TTCTGTACTA	120
AGAAAAATTC	TTCTGCCTTG	AGATGCTGTT	AATCTGTAAC	CCTAGCCCCA	ACCCTGTGCT	180
CACAGAGACA	TGTGCTGTGT	TGACTCAAGG	TTCAATGGAT	TAGGGCTAT	GCTTTGTTAA	240
AAAAGTGCTT	GAAGATAATA	TGCTTGTTAA	AAGTCATCAC	CATTCTCTAA	TCTCAAGTAC	300
CCAGGGACAC	AATACACTGC	GGAAGGCCGC	AGGGACCTCT	GTCTAGGAAA	GCCAGGTATT	360
GTCCAAGATT	TCTCCCCATG	TGATAGCCTG	AGATATGGCC	TCATGGGAAG	GGTAAGACCT	420
GACTGTCCCC	CAGCCCGACA	TCCCCCAGCC	CGACATCCCC	CAGCCCGACA	CCCGAAAAGG	480
GTCTGTGCTG	AGGAAGATTA	NTAAAAGAGG	AAGGCTCTTT	GCATTGAAGT	AAGAAGAAGG	540
CTCTGTCTCC	TGCTCGTCCC	TGGGCAATAA	AATGTCTTGG	TGTTAAACCC	GAATGTATGT	600
TCTACTTACT	GAGAATAGGA	GAAAACATCC	TAGGGCTGG	AGGTGAGACA	CCCTGGCGGC	660
ATACTGCTCT	TTAATGCACG	AGATGTTTGT	NTAATTGCCA	TCCAGGGCCA	NCCCCTTTCC	720
TTAACTTTTT	ATGANACAAA	AACTTTGTTC	NCTTTTCCTG	CGAACCTCTC	CCCCTATTAN	780
CCTATTGGCC	TGCCCATCCC	CTCCCCAAAN	GGTGAAAANA	TGTTCNTAAA	TNCGAGGGAA	840
TCCAAAACNT	TTTCCCCTTG	GTCCCCCTTC	CAACCCCGTC	CCTGGGCCNN	TTTCTCCCCC	900
AACNTGTCCC	GGNTCCTTCN	TTCCCNCCCC	CTTCCCNGAN	AAAAAACCCC	GTNTGANGGN	960
GCCCCCTCAA	ATTATAACCT	TTCCNAAACA	AANNGGTTCN	AAGGTGGTTT	GNTTCCGGTG	1020
CGGCTGGCCT	TGAGGTCCCC	CCTNCACCCC	AATTGGAAN	CCNGTTTTTT	TTATTGCCCN	1080
NTCCCC						1086

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

NCCNNTTTAGA	TGTTGACAAN	NTAAACAAGC	NGCTCAGGCA	GCTGAAAAAA	GCCACTGATA	60
AAGCATCCTG	GAGTATCAGA	GTTTACTGTT	AGATCAGCCT	CATTGACTT	CCCCTCCCAC	120
ATGGTGTTTA	AATCCAGCTA	CACTACTTCC	TGACTCAAAC	TCCACTATTC	CTGTTTCATGA	180
CTGTTCAGGAA	CTGTTGGAAA	CTACTGAAAC	TGGCCGACCT	GATCTTCAAA	ATGTGCCCCCT	240
AGGAAAGGTG	GATGCCACCG	TGTTACACAGA	CAGTACCNC	TTCCTCGAGA	AGGGACTACG	300
AGGGGCCGGT	GCANCTGTTA	CCAAGGAGAC	TNATGTGTTG	TGGGCTCAGG	CTTTACCANC	360
AAACACCTCA	NCNCNNAAGG	CTGAATTGAT	CGCCCTCACT	CAGGCTCTCG	GATGGGGTAA	420
GGGATATTAA	CGTTAACACT	GACAGCAGGT	ACGCCTTTGC	TACTGTGCAT	GTACGTGGAG	480
CCATCTACCA	GGAGCGTGGG	CTACTCACTC	GGCAGGTGGC	TGTNATCCAC	TGTAAANGGA	540
CATCAAAAGG	AAAACNNGGC	TGTTGCCCGT	GGTAACCANA	AANCTGATCN	NCAGCTCNA	600
GATGCTGTGT	TGACTTTCAC	TCNCNCCTCT	TAAACTTGCT	GCCCACANTC	TCCTTTCCCA	660
ACCAGATCTG	CCTGACAATC	CCCATACTCA	AAAAAAAAN	AANACTGGCC	CCGAACCCNA	720
ACCAATAAAA	ACGGGGGANGG	TNGGTNGANC	NNCCTGACCC	AAAAATAATG	GATCCCCCGG	780
GCTGCAGGAA	TTCAATTCAN	CCTTATCNAT	ACCCCCAACN	NGGNGGGGGG	GGCNGTNCC	840
CATTNCCCCT	NTATTNATTC	TTTNCCCCC	CCCCCGGNT	CCTTTTTNAA	CTCGTGAAAG	900
GGAAAACCTG	NCTTACCAAN	TTATCNCTG	GACNCTCCCC	TTCCNCGGTN	GNTTANAAAA	960
AAAAGCCCN	ANTCCCNCTC	NAAATTTGCA	CNGAAAGGNA	AGGAATTTAA	CCTTTATTTT	1020
TTNNTCCTTT	ANTTTGTNNN	CCCCCTTTTA	CCCAGGCGAA	CNGCCATCNT	TTAANAAAAA	1080
AAANAGAANG	TTTATTTTTC	CTTNGAACCA	TCCCAATANA	AANCAACCCG	NGGGGAACGG	1140
GGNGGNAGGC	CNCTCACCCC	CTTNTGTNG	GNGGGNC			1177

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NCCNNTTNTT	GATGTTGTCT	TTTTGGCCTC	TCTTTGGATA	CTTTCCTCT	CTTCAGAGGT	60
GAAAAGGGTC	AAAAGGAGCT	GTTGACAGTC	ATCCCAGGTG	GGCCAATGTG	TCCAGAGTAC	120
AGACTCCATC	AGTGAGGTCA	AAGCCTGGGG	CTTTTCAGAG	AAGGGAGGAT	TATGGGTTTT	180
CCAATTATAC	AAGTCAGAAG	TAGAAAGAAG	GGACATAAAC	CAGGAAGGGG	GTGGAGCACT	240
CATCACCCAG	AGGGACTTGT	GCCTCTCTCA	GTGGTAGTAG	AGGGGCTACT	TCCTCCCACC	300
ACGGTTGCAA	CCAAGAGGCA	ATGGGTGATG	AGCCTACAGG	GGACATANCC	GAGGAGACAT	360
GGGATGACCC	TAAGGGAGTA	GGCTGGTTTT	AAGGCGGTGG	GACTGGGTGA	GGGAAACTCT	420
CCTCTTCTTC	AGAGAGAAGC	AGTACAGGGC	GAGCTGAACC	GGCTGAAGGT	CGAGGCGAAA	480
ACACGGTCTG	GCTCAGGAAG	ACCTTGGAAG	TAAAATTATG	AATGGTGCAT	GAATGGAGCC	540
ATGGAAGGGG	TGCTCCTGAC	CAAACTCAGC	CATTGATCAA	TGTTAGGGAA	ACTGATCAGG	600
GAAGCCGGGA	ATTTTCATTAA	CAACCCGCCA	CACAGCTTGA	ACATTGTGAG	GTTTCAGTGAC	660
CCTTCAAGGG	GCCACTCCAC	TCCAACCTTG	GCCATTCTAC	TTTGCNAAAT	TTCCAAAACT	720
TCCTTTTTTA	AGGCCGAATC	CNTANTCCCT	NAAAAACNAA	AAAAAATCTG	CNCCTATTCT	780
GGAAAAGGCC	CANCCCTTAC	CAGGCTGGAA	GAAATTTTNC	CTTTTTTTTT	TTTTTGAAGG	840
CNTTNTTAA	ATTGAACCTN	AATTCNCCCC	CCCAAAAAAA	AACCCNCCNG	GGGGGCGGAT	900
TTCCAAAAAC	NAATTCCCTT	ACCAAAAAAC	AAAAACCCNC	CCTTNTTCCC	TTCCNCCCTN	960
TTCTTTTAAT	TAGGGAGAGA	TNAAGCCCCC	CAATTTCCNG	GNCTNGATNN	GTTTCCCCCC	1020
CCCCCATTTT	CCNAACTTTT	TTCCCANCA	GGAANCCNCC	CTTTTTTTNG	GTCNGATTNA	1080
NCAACCTTCC	AAACCATTTT	TCCNNAAAAA	NTTGTNTNGG	NGGGAAAAAN	ACCTNNTTTT	1140

ATAGAN

1146

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTCATTGGG TACGGGCCCC CTCGAGGTCG ACGGTATCGA TAAGCTTGAT ATCGAATTCC	60
TGCAGCCCGG GGGATCCACT AGTTCTAGAG TCAGGAAGAA CCACCAACCT TCCTGATTTT	120
TATTGGCTCT GAGTTCTGAG GCCAGTTTTC TTCTTCTGTT GAGTATGCGG GATTGTCAGG	180
CAGATCTGGC TGTGGAAAGG AGACTGTGGG CAGCAAGTTT AGAGGCGTGA CTGAAAGTCA	240
CACTGCATCT TGAGCTGCTG AATCAGCTTT CTGGTTACCA CGGGCAACAG CCGTGTTTTTC	300
CTTTTGATGT CCTTTACAGT GGATTACAGC CACCTGCTGA GGTGAGTAGC CCACGCTCCT	360
GGTAGATGGC TCCACGTACA TGCACAGTAG CAAAGGCGTA CCTGCTGTCA GTGTTAACGT	420
TAATATCCTT ACCCCATCGG AGAGCCTGAG TGAGGGCGAT CAATTCAGCC CTTTGTGCT	480
GAGGTGTTTG CTGGTTAAGC CCTGAACCCA CAACACATCT GTCTCCATGG TAACAGCTGC	540
ACCGG	545

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCTAGGC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
GGGGGATCG CTTGAGCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCTAT	120
CTCTACGAAA AAATAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
AATCGAGCCT AGGAGA	196

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTCCTAGGC TTGGGGGCTC TGA CTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAC TG	60
TGACACCAAC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AATAAAATAA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
TAAGTGACAT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCCAGC CTGGGATTAA	240

ACTGACAGCA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
CTCTACCGTT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCAGTCC CAAGCTCACT	360
TACTATACCT CCTTTATAGC CTAGGAGA	388

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGTAGTTGC CTATAATCAT GTTCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
TACCCTGAAA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCA ATAATTGATC	120
ACAAGATATG ATTTCTACAT CAGATGCTCT TTCCTTTCTT GTTTATTTCC TTTTATTTT	180
GGTTGTGGGG TCGAATGTAA TAGCTTTGTT TCAAGAGAGA GTTTTGGCAG TTTCTGTAGC	240
TTCTGACACT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
TGAGAGGTCT ATTTTTTCCA TATTTGGGCA ACTACTA	337

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGTAGTTGC CACACAGTGC CTTTCCATTT ATTTAACCCC CACCTGAACG GCATAAACTG	60
AGTGTTTCAAGC TGGTGTCTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AAAATCATAT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTT ACACCTCCTTA	180
AAACAGTTTT TAAGTCGTTT GGAACAAGAT ATTTTTCTT TCCTGGCAGC TTTTAACATT	240
ATAGCAAATT TGTGTCTGGG GGAAGTCTGG TCACTGTTT TCACAGTTGC AAATCAAGGC	300
ATTTGCAACC AAGAAAAAAA AATTTTTTTT TTTTATTTGA AACTGGACCG GATAAACGGT	360
GTTTGGAGCG GCTGCTGTAT ATAGTTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
TATGTGGGGG GGGGNTTTT NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTTNT	480
CTTTTGGNNA CTGAGCTAAA AAGGGCTGNT TTTCCGGTGG GGGCAGATGA AGGCTCACAG	540
GAGGCCTTTC TCTTAGAGGG GGGAACNCT A	571

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATATATTTA	ATAACTTAAA	TATATTTTGA	TCACCCACTG	GGGTGATAAG	ACAATAGATA	60
TAAAAGTATT	TCCAAAAAGC	ATAAAACCAA	AGTATCATAC	CAAACCAAAT	TCATACTGCT	120
TCCCCACCC	GCACTGAAAC	TTCACCTTCT	AACTGTCTAC	CTAACCAAAT	TCTACCCTTC	180
AAGTCTTTGG	TGCGTGCTCA	CTACTCTTTT	TTTTTTTTTT	TTTNTTTTGG	AGATGGAGTC	240
TGGCTGTGCA	GCCCAGGGGT	GGAGTACAAT	GGCACAACCT	CAGCTCACTG	NAACCTCCGC	300
CTCCCAGGTT	CATGAGATTC	TCCTGNTTCA	GCCTTCCCAG	TAGCTGGGAC	TACAGGTGTG	360
CATCACCATG	CCTGGNTAAT	CTTTTTTNGT	TTTNGGGTAG	AGATGGGGGT	TTTACATGTT	420
GGCCAGGNTG	GTNTCGAACT	CCTGACCTCA	AGTGATCCAC	CCACCTCAGG	CTCCCAAAGT	480
GCTAGGATTA	CAGACATGAG	CCACTGNGCC	CAGNCCTGGT	GCATGCTCAC	TTCTCTAGGC	540
AACTACTA						548

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCGTTATG	CACATGCAGA	ATATTCTATC	GGTACTTCAG	CTATTACTCA	TTTTGATGGC	60
GCAATCCGAG	CCTATCCTCA	AGATGAGTAT	TTAGAAAGAA	TTGATTTAGC	GATAGACCAA	120
GCTGGTAAGC	ACTCTGACTA	CACGAAATTG	TTCAGATGTG	ATGGATTTAT	GACAGTTGAT	180
CTTTGGAAGA	GATTATTAAG	TGATTATTTT	AAAGGGAATC	CATTAATTCC	AGAATATCTT	240
GGTTTAGCTC	AAGATGATAT	AGAAATAGAA	CAGAAAGAGA	CTACAAATGA	AGATGTATCA	300
CCAAGTATA	TTGAAGAGCC	TATAGTAGAA	AATGAATTAG	CTGCATTTAT	TAGCCTTACA	360
CATAGCGATT	TTCCTGATGA	ATCTTATATT	CAGCCATCGA	CATAGCATTG	CCTGATGGGC	420
AACCTTACGA	ATAATAGAAA	CTGGGTGCGG	GGCTATTGAT	GAATTCATCC	NCAGTAAATT	480
TGGATATNAC	AAAATATAAC	TCGATTGCAT	TTGGATGATG	GAATACTAAA	TCTGGCAAAA	540
GTAACCTTTG	AGCTACTAGT	AACCTCTCTT	TTTGAGATGC	AAAATTTTCT	TTTAGGGTTT	600
CTTATTCTCT	ACTTTACGGA	TATTGGAGCA	TAACGGGA			638

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGATGGAT	GTCGCCGAG	GCGAGGGGCC	TTATCTGATG	CTCGGCTGCC	TGTTTCGTGAT	60
GTGCGCGGCG	ATTGGGCTGT	TTATCTCAAA	CACCGCCACG	GCGGTGCTGA	TGGCGCCTAT	120
TGCCTTAGCG	GCGGCGAAGT	CAATGGGCGT	CTCACCTTAT	CCTTTTGCCA	TGGTGGTGGC	180
GATGGCGGCT	TCGGCGGCGT	TTATGACCCC	GGTCTCCTCG	CCGGTTAACA	CCCTGGTGTCT	240
TGGCCCTGGC	AAGTACTCAT	TTAGCGATTT	TGTCAAAATA	GCGCTG		286

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGGTCATAG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
TAGCCTTACA TTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
CATATCACAC ATAAGTCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACCTCT	180
GTGNCAAGAA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTGTTC TTNCTATTN	240
TCACTCTTCA CCTATGACCG AA	262

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGGTCATAG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
ATTTATGATA AATGGTGGCA GGATTTTTAT TATAACATG TACCCATGCA AATTCCTAT	120
AACTCTGAGA TATATTCTC TACATTTAAA CAATAAAAT AATCTATTTT TAAAGCCTA	180
ATTTGCGTAG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
CGTTTCTCTG CCTATGACCG A	261

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TACAACGAGG CGACGTCGGT AAAATCGGAC ATGAAGCCAC CGCTGGTCTT TTCGTCCGAG	60
CGATAGGCGC CGGCCAGCCA GCGGAACGGT TGCCCGGATG GCGAAGCGAG CCGGAGTTCT	120
TCGGACTGAG TATGAATCTT GTTGTGAAAA TACTCGCCGC CTTCGTTTCA CGACGTCGCG	180
TCGAAATCTT CGANCTCCTT ACGATCGAAG TCTTCGTGGG CGACGATCGC GGTCACTTCC	240
GCCCCACCGA AATCATGGTT GAGCCGGATG CTGNCCCCGA AGNCCTCGTT TGTN	294

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGGTAAAGG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
ATCAATGAAT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GTTCTCATGG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CAACTAGTCG NCTTGCNANG ATCTTCAT	208

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NCCNTTGAGC TGAGTGATTG AGATNTGTAA TGGTTGTAAG GGTGATTCAG GCGGATTAGG	60
GTGGCGGGTC ACCCGGCAGT GGGTCTCCCG ACAGGCCAGC AGGATTGGG GCAGGTACGG	120
NGTGCGCATC GCTCGACTAT ATGCTATGGC AGGCGAGCCG TGGAAGGNGG ATCAGGTCAC	180
GGCGCTGGAG CTTCCACGG TCCATGNATT GNGATGGCTG TTCTAGGCGG CTGTTGCCAA	240
CCGTGATGGT ACGCTGGCTG GAGCATTGAT TTCTGGTGCC AAGGTGG	287

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGGTAAAG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCTCG GCCTACGACT	60
GGGCCAAGCT GTCGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCCTCCG	120
NCGTTACTTC NCCGTCCAGG AGGAGGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
GATNCTCCTC ATGGTCNACA TCCC	204

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGATTGGTC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
GTCCTAAATG ATAGTTGCTG AGTTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
TTAACTTTCC AATCGCATGG ACATGTTAGA CTTATTTTCT GTTAATGATT NCTATTTTAA	180

TTAAATTGGA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG 240
ACATTATAGC TTAGTATGTG ACCA 264

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG 60
TGCACCCGCA ATCCCAGCTA CTTGGGAGGT TGAGACACAA GANTCACCTA NATGTGGGAG 120
GTCAAGGTTG CATGAGTCAT GATTGTGCCA CTGCACTCCA GCCTGGGTGA CAGACCGAGA 180
CCCTGCCTCA ANAGANAANG AATAGGAAGT TCAGAAATCN TGGNTGTGGN GCCCAGCAAT 240
CTGCATCTAT NCAACCCCTG CAGGCAANGC TGATGCAGCC TANGTTCAAG AGCTGCTGTT 300
TCTGGAGGCA GCAGTTNGGG CTTCCATCCA GTATCACGGC CACACTCGCA CNAGCCATCT 360
GTCTCCGTTN TGTNAC 376

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG 60
TGCACCTGTA ATCCCAGCTA CTTGGGCGGC TGAGACACAA GAACCACCTA AATGTGGGAG 120
GGTCAAGGTT GCATGAGTCA TGATCGCGCC ACTGCACTCC AGCCTGGGTG ACAGACTGAG 180
ACCCTGCCTC AAAAGAAAAA GAATAGGAAG TTCAGAAACC CTGGGTGTGG NGCCCAGCAA 240
TCTGCATTTA AACAATCCCT GCAGGCAATG CTGATGCAGC CTAAGTTCAA GAGCTGCTGT 300
TCTGGAGGCA GNAGTAAGGG CTTCCATCCA GCATCACGGN CAACACTGCA AAAGCACCTG 360
TCCTCGTTGG TA 372

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCTGTCCAC ATCTACAAAGT TTTATTTATT TTGTGGGTTT TCAGGGTGAC TAAGTTTTTC 60
CCTACATTGA AAAGAGAAAGT TGCTAAAAGG TGCACAGGAA ATCATTTTTT TAAGTGAATA 120
TGATAATATG GGTCCGTGCT TAATACAAC T GAGACATATT TGTTCTCTGT TTTTTTAGAG 180

TCACCTCTTA AAGTCCAATC CCACAATGGT GAAAAAAAAA TAGAAAGTAT TTGTTCTACC	240
TTTAAGGAGA CTGCAGGGAT TCTCCTTGAA AACGGAGTAT GGAATCAATC TTAAATAAAT	300
ATGAAATTGG TTGGTCTTCT GGGATAAGAA ATTCCCAACT CAGTGTGCTG AAATTCACCT	360
GACTTTTTTT GGGAAAAAAT AGTCGAAAAT GTCAATTGG TCCATAAAAT ACATGTTACT	420
ATTAAGAAGAT ATTTAAAGAC AAATTCTTTC AGAGCTCTAA GATTGGTGTG GACAGAA	477

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTNCAACCT CTTGANTGTC AAAAACCTTN TAGGCTATCT CTAAAAGCTG ACTGGTATTC	60
ATTCCAGCAA AATCCCTCTA GTTTTGGAG TTTCCTTTTA CTATCTGGGG CTGCCTGAGC	120
CACAAATGCC AAATTAAGAG CATGGCTATT TTCGGGGGCT GACAGGTCAA AAGGGGTGTA	180
AATCCGATAA GCCTCCTGGA GGTGCTCTAA AAACACTCCT GGTGACTCAT CATGCCCTG	240
GACGACTTCA ATCGNCTTAG ACAAGTTTAT AGGTTTCTGG GCAGCTCCCT GAATACCCAC	300
GAGGAGATAC CGGTGGAAAT CGTCAAAAGT TCTCCCTCCA CTTGAGAAAT TTGGGTCCCA	360
ATTAGGTCCC AATTGGGTCT CTAATCACTA TTCCTCTAGC TTCCTCCTCC GGNCTATTGG	420
TTGATGTGAG GTTGAAGA	438

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAGGGTAC CAGCCCCAAG CCTTGACAAC TTCCATAGGG TGTCAAGCCT GTGGGTGCAC	60
AGAAGTCAAA AATTGAGTTT TGGGATCCTC AGCCTAGATT TCAGAGGATA TAAAGAAACA	120
CCTAACACCT AGATATTCAG ACAAAGTTT ACTACAGGGA TGAAGCTTTC ACGGAAAACC	180
TCTACTAGGA AAGTACAGAA GAGAAATGTG GGTTTGGAGC CCCCAAACAG AATCCCCTCT	240
AGAACACTGC CTAATGAAAC TGTGAGAAGA TGGCCACTGT CATCCAGACA CCAGAATGAT	300
AGACCCACCA AAAACTTATG CCATATTGCC TATAAACCT ACAGACACTC AATGCCAGCC	360
CCATGAAAAA AAAACTGAGA AGAAGACTGT NCCCTACAAT GCCACCGGAG CAGAACTGCC	420
CCAGGCCATG GAAGCACAGC TCTTATATCA ATGTGACCTG GATGTTGAGA CATGGAATCC	480
NANGAAATCN TTTTAANACT TCCACGGTTN AATGACTGCC CTATTANATT CNGAACTTAN	540
ATCCNGGCCT GTGACCTCTT TGCTTTGGCC ATTCCCCCTT TTTGGAATGG CTNTTTTTTT	600
CCCATGCGCTG TNCCCTCTTA	620

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTACAACGAG GGGGTCAATG TCATAAATGT CACAATAAAA CAATCTCTTC TTTTTTTTTT	60
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	100

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TAGTCTATGC GCCGGACAGA GCAGAATTAA ATTGGAAGTT GCCCTCCGGA CTTTCTACCC	60
ACACTCTTCC TGAAAAGAGA AAGAAAAGAG GCAGGAAAGA GGTAGGATT TCATTTTCAA	120
GAGTCAGCTA ATTAGGAGAG CAGAGTTTAG ACAGCAGTAG GCACCCCATG ATACAAACCA	180
TGGACAAAGT CCCTGTTTAG TAACTGCCAG ACATGATCCT GCTCAGGTTT TGAAATCTCT	240
CTGCCCATAA AAGATGGAGA GCAGGAGTGC CATCCACATC AACACGTGTC CAAGAAAGAG	300
TCTCAGGGAG ACAAGGGTAT CAAAAAACAA GATTCTTAAT GGGAAGGAAA TCAAACCAA	360
AAATTAGATT TTTCTCTACA TATATATAAT ATACAGATAT TTAACACATT ATTCCAGAGG	420
TGGCTCCAGT CCTTGGGGCT TGAGAGATGG TGAAACTTT TGTTCCACAT TAACTTCTGC	480
TCTCAAATTC TGAAGTATAT CAGAATGGGA CAGGCAATGT TTTGCTCCAC ACTGGGGCAC	540
AGACCCAAAT GGTCTGTGTC CCGAAGAAGA GAAGCCCGAA AGACATGAAG GATGCTTAAG	600
GGGGGTTGGG AAAGCCAAAT TGGTANTATC TTTTCCTCCT GCCTGTGTTC CNGAAGTCTC	660
CNCTGAAGGA ATTCTTAAAA CCCTTTGTGA GGAAATGCCC CCTTACCATG ACAANTGGTC	720
CCATTGCTTT TAGGGNGATG GAAACACCAA GGGTTTGTAT CC	762

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGTCTATGC GTGTATTAACT CCCCCTCCC TCAGTAACAA CCAAAGAGGC AGGAGCTGTT	60
ATTACCAACC CCATTTTACA GATGCATCAA TAATGACAGA GAAGTGAAGT GACTTGCGCA	120
CACAACCAGT AAATTGGCAG AGTCAGATTT GAATCCATGG AGTCTGGTCT GCACTTTCAA	180
TCACCGAATA CCCTTTCTAA GAAACGTGTG CTGAATGAGT GCATGGATAA ATCAGTGTCT	240
ACTCAACATC TTTGCCTAGA TATCCCGCAT AGACTA	276

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TAGTAGTTGC	CAAATATTTG	AAAATTTACC	CAGAAGTGAT	TGAAAACTTT	TTGGAAACAA	60
AAACAAATAA	AGCCAAAAGG	TAAAATAAAA	ATATCTTTGC	ACTCTCGTTA	TTACCTATCC	120
ATAACTTTTT	CACCGTAAGC	TCTCCTGCTT	GTTAGTGTAG	TGTGGTTATA	TTAAACTTTT	180
TAGTTATTAT	TTTTTATTCA	CTTTTCCACT	AGAAAGTCAT	TATTGATTTA	GCACACATGT	240
TGATCTCATT	TCATTTTTC	TTTTTATAGG	CAAAATTTGA	TGCTATGCAA	CAAAAATACT	300
CAAGCCCAT	ATCTTTTTC	CCCCCGAAAT	CTGAAAATTG	CAGGGGACAG	AGGGAAGTTA	360
TCCCATTAAA	AAATTGTAAA	TATGTTTCAGT	TTATGTTTAA	AAATGCACAA	AACATAAGAA	420
AATTGTGTTT	ACTTGAGCTG	CTGATTGTAA	GCAGTTTAT	CTCAGGGGCA	ACTACTA	477

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTAGTTGC	CAATTCAGAT	GATCAGAAAT	GCTGCTTTC	TCAGCATTGT	CTTGTTAAAC	60
CGCATGCCAT	TTGGAACTTT	GGCAGTGAGA	AGCCAAAAGG	AAGAGGTGAA	TGACATATAT	120
ATATATATAT	ATTCAATGAA	AGTAAAATGT	ATATGCTCAT	ATACTTTCTA	GTTATCAGAA	180
TGAGTTAAGC	TTTATGCCAT	TGGGCTGCTG	CATATTTTAA	TCAGAAGATA	AAAGAAAATC	240
TGGGCATTTT	TAGAATGTGA	TACATGTTTT	TTTAAACTG	TTAAATATTA	TTTCGATATT	300
TGTCTAAGAA	CCGGAATGTT	CTTAAAATTT	ACTAAACAG	TATTGTTTGA	GGAAGAGAAA	360
ACTGTACTGT	TTGCCATTAT	TACAGTCGTA	CAAGTGCATG	TCAAGTCACC	CACTCTCTCA	420
GGCATCAGTA	TCCACCTCAT	AGCTTTACAC	ATTTTGACGG	GGAATATTGC	AGCATCCTCA	480
GGCCTGACAT	TGGGGAAGG	CTCAGATCCA	CCTACTGCTC	CTTGCTCGTT	GATTTGTTTT	540
AAAATATTGT	GCCTGGTGTC	ACTTTTAAGC	CACAGCCCTG	CCTAAAAGCC	AGCAGAGAAC	600
AGAACCCGCA	CCATTCTATA	GGCAACTACT	A			631

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TAGTAGTTGC	CATCCCATAT	TACAGAAGGC	TCTGTATACA	TGACTTATTT	GGAAGTGATC	60
TGTTTTCTCT	CCAAACCCAT	TTATCGTAAT	TTACCAGTC	TTGGATCAAT	CTTGGTTTCC	120
ACTGATACCA	TGAAACCTAC	TTGGAGCAGA	CATTGCACAG	TTTTCTGTGG	TAAAACTAA	180
AGGTTTATTT	GCTAAGCTGT	CATCTTATGC	TTAGTATTTT	TTTTTTACAG	TGGGGAATTG	240
CTGAGATTAC	ATTTTGTTAT	TCATTAGATA	CTTTGGGATA	ACTTGACACT	GTCTTCTTTT	300
TTTCGCTTTT	AATTGCTATC	ATCATGCTTT	TGAAACAAGA	ACACATTAGT	CCTCAAGTAT	360

TACATAAGCT	TGCTTGTTAC	GCCTGGTGGT	TTAAAGGACT	ATCTTTGGCC	TCAGGTTTAC	420
AAGAATGGGC	AAAGTGTTC	CTTATGTTCT	GTAGTTCTCA	ATAAAAGATT	GCCAGGGGCC	480
GGGTACTGTG	GCTCGCACTG	TAATCCCAAGC	ACTTTGGGAA	GCTGAGGCTG	GCGGATCATG	540
TTAGGGCAGG	TGTTCGAAAC	CAGCCTGGGC	AACTACTA			578

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGTAGTTGC	CTGTAATCCC	AGCAACTCAG	GAGGCTGGGG	CAGGAGAATC	AGTTGAACCT	60
GGGAGGCAGA	AGTTGTAATT	AGCAAAGATC	GCACCATTGC	ACTTCAGCCT	GGGCAACAAG	120
AGTGAGATTC	CATCTCAAAA	ACAAAAA	GAAAAAGAAA	AGAAAAGGAA	AAAACGTATA	180
AACCCAGCCA	AAACAAAATG	ATCATTCTTT	TAATAAGCAA	GACTAATTTA	ATGTGTTTAT	240
TTAATCAAAG	CAGTTGAATC	TTCTGAGTTA	TTGGTGAAAA	TACCCATGTA	GTTAATTTAG	300
GTTTCTTACT	TGGGTGAACG	TTTGATGTTT	ACAGGTTATA	AAATGGTTAA	CAAGGAAAAT	360
GATGCATAAA	GAATCTTATA	AACTACTAAA	AATAAATAAA	ATATAAATGG	ATAGGTGCTA	420
TGGATGGAGT	TTTTGTGTAA	TTTAAAATCT	TGAAGTCATT	TTGGATGCTC	ATTGGTTGTC	480
TGGTAATTTT	CATTAGGAAA	AGGTTATGAT	ATGGGGAAAC	TGTTTCTGGA	AATTGCGGAA	540
TGTTTCTCAT	CTGTAAAATG	CTAGTATCTC	AGGGCAACTA	CTA		583

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCTACTAG	TCATNTGGAT	TCTATCCATG	GCAGCTAAGC	CTTTCTGAAT	GGATTCTACT	60
GCTTTCTTGT	TCTTTAATCC	AGACCCTTAT	ATATGTTTAT	GTTCACAGGC	AGGGCAATGT	120
TTAGTGAAAA	CAATTCTAAA	TTTTTTATTT	TGCATTTTCA	TGCTAATTTT	CGTCACACTC	180
CAGCAGGCTT	CCTGGGAGAA	TAAGGAGAAA	TACAGCTAAA	GACATTGTCC	CTGCTTACTT	240
ACAGCCTAAT	GGTATGCAAA	ACCACTTCAA	TAAAGTAACA	GGAAAAGTAC	TAACCAGGTA	300
GAATGGACCA	AAACTGATAT	AGAAAAATCA	GAGGAAGAGA	GGAACAAATA	TTTACTGAGT	360
CCTAGAATGT	ACAAGGCTTT	TTAATTACAT	ATTTTATGTA	AGGCCTGCAA	AAAACAGGTG	420
AGTAATCAAC	ATTTGTCCCA	TTTACATAT	AAGGAACTG	AAGCTTAAAT	TGAATAATTT	480
AATGCATAGA	TTTTATAGTT	AGACCATGTT	CAGGTCCCTA	TGTTATACTT	ACTAGCTGTA	540
TGAATATGAG	AAAATAATTT	TGTTATTTTC	TTGGCATCAG	TATTTTCATC	TGCAAAATAA	600
AGCTAAAGTT	ATTTAGCAAA	CAGTCAGCAT	AGTGCCTGAT	ACATAGTAGG	TGCTCCAAAC	660
ATGATTACNC	TANTATTNGG	TATTANAAAA	ATCCAATATA	GGCNTGGATA	AAACCG	716

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTCTGTCCAC ATATCATCCC ACTTTAATTG TTAATCAGCA AACTTTTCAA TGAAAAATCA	60
TCCATTTTAA CCAGGATCAC ACCAGGAAAC TGAAGGTGTA TTTTTTTTCTA CCTTAAAAAA	120
AAAAAAAAAA ACCAAACAAA CCAAAACAGA TTAACAGCAA AGAGTTCTAA AAAATTTACA	180
TTTCTCTTAC AACTGTCATT CAGAGAACAA TAGTTCTTAA GTCTGTATAA TCTTGGCATT	240
AACAGAGAAA CTTGATGAAN AGTTGTACTT GGAATATTGT GGATTTTTTT TTTTGTCTAA	300
TCTCCCCCTA TTGTTTTGCC AACAGTAATT TAAGTTTGTG TGGAACATCC CCGTAGTTGA	360
AGTGTAACA ATGTATAGGA AGGAATATAT GATAAGATGA TGCATCACAT ATGCATTACA	420
TGTAGGGACC TTCACAACCT CATGCACTCA GAAAACATGC TTGAAGAGGA GGAGAGGACG	480
GCCCAGGGTC ACCATCCAGG TGCCTTGAGG ACAGAGAATG CAGAAGTGGC ACTGTTGAAA	540
TTTAGAAGAC CATGTGTGAA TGGTTTCAGG CCTGGGATGT TTGCCACCAA GAAGTGCCCTC	600
CGAGAAATTT CTTTCCCATT TGGAAATACAG GGTGGCTTGA TGGGTACGGT GGGTGACCCA	660
ACGAAGAAAA TGAAATTCTG CCCTTTCC	688

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TAGTAGTTGC CGCNNACCTA AAANTTGGAA AGCATGATGT CTAGGAAACA TANTAAAATA	60
GGGTATGCCT ATGTGCTACA GAGAGATGTT AGCATTTAAA GTGCATANTT TTATGTATTT	120
TGACAAATGC ATATNCCTCT ATAATCCACA ACTGATTACG AAGCTATTAC AATTAAAAAG	180
TTTGGCCGGG CGTGGTGGGC GGTGGCTGAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA	240
GGCACGCGGA TCACGAGGTC GGGAGTTCAA GACCATCCTG GCTAACACGG TGAAAGTCCA	300
TCTCTACTAA AAATACGAAA AAATTACCCC GGCGTGGTGG CGGGCGCCTG TAGTCCCAGC	360
TACTCCGGAG GCTGAGGCAG GAGAATGGCG TGAACCCAGG ACACGGAGCT TGCAGTGTGC	420
CAACATCACG TCACTGCCCT CCAGCCTGGG GGACAGGAAC AAGANTCCCG TCCTCANAAA	480
AGAAAAATAC TACTNATANT TTCNACTTTA TTTTAANTTA CACAGAACTN CCTCTTGCTA	540
CCCCCTTACC ATTCATCTCA CCCACCTCCT ATAGGGCACN NCTAA	585

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCTGTCCACA CCAATCTTAG AAGCTCTGAA AAGAATTTGT CTTTAAATAT CTTTAAATAG	60
TAACATGTAT TTTATGGACC AAATTGACAT TTTCGACTGT TTTTCCAAA AAAGTCAGGT	120

GAATTTTCAGC	ACACTGAGTT	GGGAATTTCT	TATCCCAGAA	GACCAACCAA	TTTCATATTT	180
ATTTAAGATT	GATTCCATAC	TCCGTTTTCA	AGGAGAATCC	CTGCAGTCTC	CTTAAAGGTA	240
GAACAAATAC	TTCCTATTTT	TTTTTCACCA	TTGTGGGATT	GGACTTTAAG	AGGTGACTCT	300
AAAAAAACAG	AGAACAAATA	TGTCTCAGTT	GTATTAAGCA	CGGACCCATA	TTATCATATT	360
CACTTAAAAA	AATGATTTCC	TGTGCACCTT	TTGGCAACTT	CTCTTTTCAA	TGTAGGGAAA	420
AACTTAGTCA	CCCTGAAAAC	CCACAAAATA	AATAAAACTT	GTAGATGTGG	ACAGA	475

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAAGAGGGTA	CATCGGGTAA	GAACGTAGGC	ACATCTAGAG	CTTAGAGAAG	TCTGGGGTAG	60
GAACAAAATC	TAAGTATTTA	TAAGGGTATA	GGTAACATTT	AAAAGTAGGG	CTAGCTGACA	120
TTATTTAGAA	AGAACACATA	CGGAGAGATA	AGGGCAAAGG	ACTAAGACCA	GAGGAACACT	180
AATATTTAGT	GATCACTTCC	ATTCTTGGTA	AAAATAGTAA	CTTTTAAGTT	AGCTTCAAGG	240
AAGATTTTTG	GCCATGATTA	GTTGTCAAAA	GTTAGTTCTC	TTGGGTTTAT	ATTACTAATT	300
TTGTTTAAAG	ATCCTTGTTA	GTGCTTTAAT	AAAGTCATGT	TATATCAAAC	GCTCTAAAC	360
ATTGTAGCAT	GTAAATGTC	ACAATATACT	TACCATTTGT	TGTATATGGC	TGTACCTCT	420
CTA						423

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCCTAGGC	TAATGTGTGT	GTTTCTGTAA	AAGTAAAAAG	TTAAAAATTT	TAAAAATAGA	60
AAAAAGCTTA	TAGAATAAGA	ATATGAAGAA	AGAAAATATT	TTGTACATT	TGCACAATGA	120
GTTTATGTTT	TAAGCTAAGT	GTTATTACAA	AAGAGCCAAA	AAGGTTTTAA	AAATTAAAC	180
GTTTGTAAG	TTACAGTACC	CTTATGTAA	TTTATAATTG	AAGAAAGAAA	AACTTTTTTT	240
TATAAATGTA	GTGTAGCCTA	AGCATACAGT	ATTTATAAAG	TCTGGCAGTG	TTCAATAATG	300
TCCTAGGCCT	TCACATTCAC	TACTGACTC	ACCCAGAGCA	ACTTCCAGTC	CTGTAAGCTC	360
CATTCGTGGT	AAGTGCCCTA	TACAGGTGCA	CCATTTATTT	TACAGTATTT	TTACTGTACC	420
TTCTCTATGT	TTCCATATGT	TTGATATAC	AAATACCACT	GGTTACTATN	GCCCNACAGG	480
TAATTCCAGT	AACACGGCCT	GTATACGTCT	GGTANCCCTA	GNGAAGA		527

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTCAACCT	CGTAGGACAA	CTCTCATATG	CCTGGGCACT	ATTTTtaggt	TACTACCTTG	60
GCTGCCCTTC	TTTAAGAAAA	AAAAAAGAAG	AAAAAAGAAC	TTTTCCACAA	GTTTCTCTTC	120
CTCTAGTTGG	AAAATTAGAG	AAATCATGTT	TTTAATTTTG	TGTTATTTCA	GATCACAAAT	180
TCAAACACTT	GTAAACATTA	AGCTTCTGTT	CAATCCCCTG	GGAAGAGGAT	TCATTCTGAT	240
ATTTACGGTT	CAAAAGAAGT	TGTAATATTG	TGCTTGGAAC	ACAGAGAACC	AGTTATTAAC	300
TTCTACTAC	TATTATATAA	TAAATAATAA	C			331

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCTTAGTAG	TTGCCAGGCA	AAATARCGTT	GATTCTCCTC	AGGAGCCACC	CCCAACACCC	60
CTGTTTGCTT	CTAGACCTAT	ACCTAGACTA	AAGTCCCAGC	AGACCCCTAG	AGGTGAGGTT	120
CAGAGTGACC	CTTGAGGAGA	TGTGCTACAC	TAGAAAAGAA	CTGCTTGAGT	TTTCTAATTT	180
ATATAAGCAG	AAATCTGGAG	AAGACTCATA	GGAATGGATA	TTAAGGGTGT	GAGATAATGG	240
CGGAAGGAAT	ATAGAGTTGG	ATCAGGCTGG	ACTTATTGAT	TTGAACCCAC	TAAGTAGAGA	300
TTCTGCTTTT	GATGTTGCAG	CTCAGGGAGT	TAAAAAAGGT	TTTAATGGTT	CTAATAGTTT	360
ATTTGCTTGG	TTAGCTGAAA	TATGGATAAA	AGATGGCCCA	CTGTGAGCAA	GCTGGAAATG	420
CCTGATCTCT	CTCAGTTTAA	TGTAGAGGAA	GGGATCCAAA	AGTTTAGGGA	GANTTGGATG	480
CTGGRAKTGG	ATTGGTCACT	TTGRGACCTA	CCCWTCCCAG	CTGGGAGGGT	CCAGAAGATA	540
CACCCTTGAC	CAACGCTTTG	CGAAATGGAT	TTGTGATGGC	GGCAACTACT	AA	592

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCTTAGTAG	TTGCCATTGC	GAGTGCTTGC	TCAACGAGCG	TTGAACATGG	CGGATTGTCT	60
AGATTCAACG	GATTTGAGTT	TTACCAGCAA	AGCGAACCAA	GCGCGGCCCA	GAGAATTATG	120
GGTTGGTTGG	CTTTGAAAAG	ATGGAAATCC	TGTAGGCCCTA	GTCAGAAAAG	CCTTCTTGCA	180
GAACAGTTGG	TTCTCGGGCG	AACGCTCATC	AAGATGCCCA	TTGGAAAGGC	TAGCGTGTAT	240
TTGGGAGAGC	CTGATAGCGT	GTCTTCTGAT	GATGTTTGTG	CTTGGACAGT	GACAAAAGAT	300
ATGCAAAGCA	AGTCCGAAGT	AGACGTCAAG	CTTCGTGAGC	AAATTATTGT	AGACTCCTAC	360
TTATACTGTG	AGGAATGATA	GCCAAGGGTG	GGGACTTTAA	GAATAAGGTG	GTTTGTACTT	420
GCGCCGATGA	TCCCAGGCAG	AAAGAMCTGA	TCGCTAGTTT	TATACGGGCA	ACTACTAAGC	480
CGAATTCCAG	CACACTGGCG	GCCGTTACTA	ATTGGATCCG	ANCTCGGTAC	CAGCTTGATG	540
CATASCTTGA	GTTWTCTATA	NTGTCNC				567

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAGCGAAAGA	CCGAGGGCAG	NGNNTANGNG	CGANGAAGCG	GAGAGGGCCA	AAAAGCAACC	60
GCTTTCCCCG	GGGGGTGCCG	ATTCATTAAG	GCAGGTGGAG	GACAGGTTTC	CCGATGGAAG	120
GCGGCAGGGG	CGCAAGCAAT	TAATGTGAGT	AGGCCATTCA	TTAGCACCCG	GGCTTAACAT	180
TTAAGCTTCG	GGTTGGTATG	TGGTGGGAAT	TGTGAGCGGA	TAACAATTTC	ACACAGGAAA	240
CAGCTATGAC	CATGATTACG	CCAAGCTATT	TAGGTGACAT	TATAGAATAA	CTCAAGTTAT	300
GCATCAAGCT	TGGTACCGAG	TTCGGATCCA	CTAGTAACGG	CCGCCAGTGT	GTGGAATTCG	360
GCTTAGTAGT	TGCCGACCAT	GGAGTGCTAC	CTAGGCTAGA	ATACCTGAGY	TCCTCCCTAG	420
CCTCACTCAC	ATTAAATTGT	ATCTTTTCTA	CATTAGATGT	CCTCAGCGCC	TTATTTCTGC	480
TGGACWATCG	ATAAATTAAT	CCTGATAGGA	TGATAGCAGC	AGATTAATTA	CTGAGAGTAT	540
GTTAATGTGT	CATCCCTCCT	ATATAACGTA	TTTGCATTTT	AATGGAGCAA	TTCTGGAGAT	600
AATCCCTGAA	GGCAAAGGAA	TGAATCTTGA	GGGTGAGAAA	GCCAGAATCA	GTGTCCAGCT	660
GCAGTTGTGG	GAGAAGGTGA	TATTATGTAT	GTCTCAGAA	TGACACCATA	TGGGCAACTA	720
CTAAGCCCCG	ATTCCAGCAC	ACTGGCGGGC	GTTACTAATG	GATCCGAGCT	CGGTACCAAG	780
CTTGATGCAT	AGCTTGAGTA	TCTATAGTGT	CACTAAATAG	CCTGGCGTTA	TCATGGTCAT	840
AGCTGTTTCC	TGTGTGAAAT	TGTTATCCGC	TCCCAATTCC	CCCCACCATA	CGAGCCGGAA	900
CATAAAGT						908

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGCCAACAAAG	GAAAGTTTTA	AATTTCCCCT	TGAGGATTCT	TGGTGATCAT	CAAATTCAGT	60
GGTTTTTAAG	GTTGTTTTCT	GTCAAATAAC	TCTAACTTTA	AGCCAAACAG	TATATGGAAG	120
CACAGATAKA	ATATTACACA	GATAAAAGAG	GAGTTGATCT	AAAGTARAGA	TAGTTGGGGG	180
CTTTAATTTT	TGGAACCTAG	GTCTCCCCAT	CTTCTTCTGT	GCTGAGGAAC	TTCTTGGAAG	240
CGGGGATTCT	AAAGTTCTTT	GGAAGACAGT	TTGAAAACCA	CCATGTTGTT	CTCAGTACCT	300
TTATTTTTTA	AAAGTAGGTG	AACATTTTGA	GAGAGAAAAG	GGCTTGTTG	AGATGAAGTC	360
CCCCCCCCC	CTTTTTTTTT	TTTGTAGCTGA	AATAGATACC	CTATGTTNAA	RGAARGGATT	420
ATTATTTACC	ATGCCAYTAR	SCACATGCTC	TTTGATGGGC	NYCTCCSTAC	CCTCCTTAAG	480

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGAGGGTAC	CGAGTGGAAT	TTCCGCTTCA	CTAGTCTGGT	GTGGCTAGTC	GGTTTCGTGG	60
TGGCCAACAT	TACGAACTTC	CAACTCAACC	GTTCTTGGAC	GTTCAAGCGG	GAGTACCGGC	120
GAGGATGGTG	GCGTGAATTC	TGGCCTTTCT	TTGCCGTGGG	ATCGGTAGCC	GCCATCATCG	180
GTATGTTTAT	CAAGATCTTC	TTACTAACC	CGACCTCTCC	GATTTACCTG	CCCGAGCCGT	240
GGTTTAACGA	GGGGAGGGGG	ATCCAGTCAC	GCGAGTACTG	GTCCCAGATC	TTCGCCATCG	300
TCGTGACAAT	GCCTATCAAC	TTCGTCGTCA	ATAAGTTGTG	GACCTTCCGA	ACGGTGAAGC	360
ACTCCGAAAA	CGTCCGGTGG	CTGCTGTGCG	GTGACTCCCA	AAATCTTGAT	AACAACAAGG	420
TAACCGAATC	GCGCTAAGGA	ACCCCGGCAT	CTCGGGTACT	CTGCATATGC	GTACCCCTTA	480
AGCCGAATTC	CAGCACACTG	GCGGCCGTTA	CTAATTGGAT	CCGAACTCCG	TAACCAAGCC	540
TGATGCGTAA	CTTGAGTTAT	TCTATAGTGT	CCCTAAAATA	ACCTGGCGTT	A	591

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAGAGGGTAC	CTGCCTTGAA	ATTTAAATGT	CTAAGGAAAR	TGGGAGATGA	TTAAGAGTTG	60
GTGTGGCYTA	GTCACACCAA	AATGTATTTA	TTACATCCTG	CTCCTTTCTA	GTTGACAGGA	120
AAGAAAGCTG	CTGTGGGGAA	AGGAGGGATA	AATACTGAAG	GGATTTACTA	AACAAATGTC	180
CATCACAGAG	TTTTTCCTTTT	TTTTTTTTTG	AGACAGAGTC	TTGCTCTGTC	ACCCAGGCTG	240
GAATGAAGWG	GTATGATCTC	AGTTGAATGC	AACCTCTACC	TCCTAGGTTC	AAGCGATTCT	300
CATGCCTCAG	CCTCCTGAGC	AGCTGGGACT	ATAGGCGCAT	GCTACCATGC	CAGGCTAATT	360
TTTATATTTT	TATTAGAGAC	GGGGTGTGTC	CATGTTGGCC	AGGCAGGTCT	CGAACTCCTG	420
GGCCTCAGAT	GATCTGCCCC	ACCGTACCCT	CTTA			454

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAGAGGGTAC	CAAAAAAAG	AAAAAGGAAA	AAAAGAAAAA	CAACTTGTAT	AAGGCTTTCT	60
GCTGCATACA	GCTTTTTTTT	TTTAAATAAA	TGGTGCCAAC	AAATGTTTTT	GCATTCACAC	120
CAATTGCTGG	TTTTGAAATC	GTA CTCTTCA	AAGGTATTTG	TGCAGATCAA	TCCAATAGTG	180
ATGCCCCGTA	GGTTTTGTGG	ACTGCCCCAG	TTGTCTACCT	TCTCATGTAG	GAGCCATTGA	240
GAGACTGTTT	GGACATGCCT	GTGTTTCATGT	AGCCGTGATG	TCCGGGGGGC	GTGTACATCA	300
TGTTACCGTG	GGGTGGGGTC	TGCATTGGCT	GCTGGGCATA	TGGCTGGGTG	CCCATCATGC	360
CCATCTGCAT	CTGCATAGGG	TATTGGGGCG	TTTGATCCAT	ATAGCCATGA	TTGCTGTGGT	420
AGCCACTGTT	CATCATTGGC	TGGGACATGC	TGTTACCCCTC	TTA		463

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTCAACCTC CCAAAGTGCT GGGATTACAG GACTGAGCCA CCACGCTCAG CCTAAGCCTC	60
TTTTTCACTA CCCTCTAAGC GATCTACCAC AGTGATGAGG GGCTAAAGAG CAGTGCAATT	120
TGATTACAAT AATGGAACCT AGATTTATTA ATTAACAATT TTTCCTTAGC ATGTTGGTTC	180
CATAATTATT AAGAGTATGG ACTTACTTAG AAATGAGCTT TCATTTTAAG AATTTTCATCT	240
TTGACCTTCT CTATTAGTCT GAGCAGTATG ACACTATACG TATTTTATTT AACTAACCTA	300
CCTTGAGCTA TTACTTTTAA AAAGGCTATA TACATGAATG TGTATTGTCA ACTGTAAAGC	360
CCCACAGTAT TTAATTATAT CATGATGTCT TTGAGGTTG	399

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTCAACCTC AATCAACCTT GGTAATTGAT AAAATCATCA CTTAACTTTC TGATATAATG	60
GCAATAATTA TCTGAGAAAA AAAAGTGGTG AAAGATTAAA CTTGCATTTC TCTCAGAATC	120
TTGAAGGATA TTTGAATAAT TCAAAAGCGG AATCAGTAGT ATCAGCCGAA GAAACTCACT	180
TAGCTAGAAC GTTGGACCCA TGGATCTAAG TCCCTGCCCT TCCACTAACC AGCTGATTGG	240
TTTTGTGTAA ACCTCCTACA CGCTTGGGCT TGGTCGCCTC ATTTGTCAAA GTAAAGGCTG	300
AAATAGGAAG ATAATGAACC GTGTCTTTTT GGTCTCTTTT CCATCCATTA CTCTGATTTT	360
ACAAAGAGGC CTGTATTCCC CTGGTGAGGT TG	392

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTGGGGTGAT GCCTCCTCAG GCTACAGTGA AGACTGGATT ACAGAAAGGT GCCAGCGAGA	60
TTTCAGATTCT CTGTAAACCT CTAAAGAAAA GGAGTCGCGC CTCAACTGAT GTAGAAATGA	120
CTAGTTCAGC ATACNGAGAC ACNTCTGACT CCGATTCTAG AGGACTGAGT GACCTGCAN	179

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
TTCGGGTGAT GCCTCCTCAG GCTACATCAT NATAGAAGCA AAGTAGAANA ATCNNGTTTG      60
TGCATTTTCC CACANACAAA ATTCAAATGA NTGGAAGAAA TTGGGANAGT AT      112
```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
TGAGCTTCCG CTCTGACAA CTCAATAGAT AATCAAAGGA CAACTTTAAC AGGGATTCAC      60
AAAGGAGTAT ATCCAAATGC CAATAAACAT ATAAAAAGGA ATTCAGCTTC ATCATCATCA      120
GAAGWATGCA AATTAAAACC ATAATGAGAA ACCACTATGT CCCACTAGAA TAGATAAAAT      180
CTTAAAGAC TGGTAAAACC AAGTGTGTTG AAGGCAAGAG GAGCA      225
```

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GCTCCTCTTG CTTACCAAC ACATTCTCAA AAACCTGTGA GAGTCCTAAG CATTCTCCTG      60
TTAGTATTGG GATTTTACCC CTGTCCTATA AAGATGTTAT GTACCAAAAA TGAAGTGGAG      120
GGCCATACCC TGAGGGAGGG GAGGGATCTC TAGTGTGTC AGAAGCGGAA GCTCA      175
```

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
AGCCATTTAC CACCCATGGA TGAATGGATT TTGTAATTCT AGCTGTTGTA TTTGTGAAT      60
```

TTGTTAATTT TGTTGTTTTT CTGTGAAACA CATACTTGG ATATGGGAGG TAAAGGAGTG	120
TCCAGTTGC TCCTGGTCAC TCCCTTTATA GCCATTACTG TCTTGTCTTCT TGTAACCTCAG	180
GTTAGGTTTT GGTCTCTCTT GCTCCACTGC AAAAAAAAAA AAA	223

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTTCTGAAGGT GAACGTGTAG GTAGCGGATC TCACAACTGG GGAAGTGTCA AAGACGAATT	60
AACTGACTTG GATCAATCAA ATGTGACTGA GGAAACACCT GAAGGTGAAG AACATCATCC	120
AGTGGCAGAC ACTGAAAATA AGGAGAATGA AGTTGAAGAG GTAAAAGAGG AGGGTCCAAA	180
AGAGATGACT TTGGATGGGT GGTAAATGGC T	211

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCTCCTCTTG CCTTACCAAC TTTGCACCCA TCATCAACCA TGTGGCCAGG TTTGCAGCCC	60
AGGCTGCACA TCAGGGGACT GCCTCGCAAT ACTTCATGCT GTTGCTGCTG ACTGATGGTG	120
CTGTGACGGA TGTGGAAGCC ACACGTGAGG CTGTGGTGCG TGCCTCGAAC CTGCCCATGT	180
CAGTGATCAT TATGGGTGGT AAATGGCT	208

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGCCATTTAC CACCCATACT AAATTCTAGT TCAAACCTCCA ACTTCTTCCA TAAAACATCT	60
AACCACTGAC ACCAGTTGGC AATAGCTTCT TCCTTCTTTA ACCTCTTAGA GTATTTATGG	120
TCAATGCCAC ACATTTCTGC AACTGAATAA AGTTGGTAAG GCAAGAGGAG C	171

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGTGATGC CTCCTCAGGC TTTGGTGTGT CCACTCNACT CACTGGCCTC TTCTCCAGCA	60
ACTGGTGAAN ATGTCCTCAN GAAAANCNCC ACACGCNGCT CAGGGTGGGG TGGGAANCAT	120
CANAATCATC NGGC	134

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGAGGGTACA TATGCAACAG TATATAAAGG AAGAAGTGCA CTGAGAGGAA CTTTCATCAAG	60
GCCATTTAAT CAATAAGTGA TAGAGTCAAG GCTCAACCCA GGTGTGACGG ATTCCAGGTC	120
CCAAGCTCCT TACTGGTACC CTCTT	145

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGCACTGAGA GGAATTCAAA GGGTTTATGC CAAAGAACAA ACCAGTCCTC TGCAGCCTAA	60
CTCATTTGTT TTTGGGCTGC GAAGCCATGT AGAGGGCGAT CAGGCAGTAG ATGGTCCCTC	120
CCACAGTCAG CGCCATGGTG GTCCGGTAAA GCATTTGGTC AGGCAGGCCT CGTTTCAGGT	180
AGACGGGCAC ACATCAGCTT TCTGGAAAAA CTTTTGTAGC TCTGGAGCTT TGTTTTTCCC	240
AGCATAATCA TACTACTGTGG AATCGGAGGT CAGTTTAGTT GGTAAGGCAA GAGGAGC	297

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCACTGAGAG GAACTTCCAA TACTATGTTG AATAGGAGTG GTGAGAGAGG GCATCCTTGT	60
---	----

CTTGTGCCGG	TTTTCAAAGG	GAATGCTTCC	AGCTTTTGCC	CATTCAGTAT	AATATTAAAG	120
AATGTTTTAC	CATTTTCTGT	CTTGCCTGTT	TTTCTGTGTT	TTTGTTGGTC	TCTTCATTCT	180
CCATTTTGTAG	GCCTTTACAT	GTTAGGAATA	TATTTCTTTT	AATGATACTT	CACCTTTGGT	240
ATCTTTTGTG	AGACTCTACT	CATAGTGTGA	TAAGCACTGG	GTTGGTAAGG	CAAGAGGAGC	300

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTCCTCTTG	CCTTACCAAC	TCACCCAGTA	TGTCAGCAAT	TTATCRGCT	TTACCTACGA	60
AACAGCCTGT	ATCCAAACAC	TTAACACACT	CACCTGAAAA	GTTCAGGCAA	CAATCGCCTT	120
CTCATGGGTC	TCTCTGCTCC	AGTTCTGAAC	CTTTCTCTTT	TCCTAGAACA	TGCATTTARG	180
TCGATAGAAG	TTCTCTCAG	TGC				203

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TACGGGGACC	CCTGCATTGA	GAAAGCGAGA	CTCACTCTGA	AGCTGAAATG	CTGTTGCCCT	60
TGCAGTGCTG	GTAGCAGGAG	TTCTGTGCTT	TGTGGGGCTAA	GGCTCCTGGA	TGACCCCTGA	120
CATGGAGAAG	GCAGAGTTGT	GTGCCCCCTC	TCATGGCCCTC	GTCAAGGCAT	CATGGACTGC	180
CACACACAAA	ATGCCGTTTT	TATTAACGAC	ATGAAATTGA	AGGAGAGAAC	ACAATTCACT	240
GATGTGGCTC	GTAACCATGG	ATATGGTCAC	ATACAGAGGT	GTGATTATGT	AAAGGTTAAT	300
TCCACCCACC	TCATGTGGAA	ACTAGCCTCA	ATGCAGGGGT	CCCA		344

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACTGAGAG	GAACCTCGTA	GGGAGGTTGA	ACTGGCTGCT	GAGGAGGGGG	AACAACAGGG	60
TAACCAGACT	GATAGCCATT	GGATGGATAA	TATGGTGGTT	GAGGAGGGAC	ACTACTTATA	120
GCAGAGGGTT	GTGTATAGCC	TGAGGAGGCA	TCACCCG			157

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCACTGAGAG GAACTTCTAG AAAGTGAAAG TCTAGACATA AAATAAAATA AAAATTTAAA 60
 ACTCAGGAGA GACAGCCCAG CACGGTGGCT CAGCCTGTA ATCCCAGAAC TTTGGGAGCC 120
 TGAGGAGGCA TCACCCG 137

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGGGTGATGC CTCCTCAGGC TGTATTTTGA AGACTATCGA CTGGACTTCT TATCAACTGA 60
 AGAATCCGTT AAAAATACCA GTTGTATTAT TTCTACCTGT CAAAATCCAT TTCAAATGTT 120
 GAAGTTCCTC TCAGTGC 137

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGCATGTTGA GCCCAGACAC GCAATCTGAA TGAGTGTGCA CCTCAAGTAA ATGTCTACAC 60
 GCTGCCTGGT CTGACATGGC ACACCATCNC GTGGAGGGCA CASCTCTGCT CNGCCTACWA 120
 CGAGGGCANT CTCATWGACA GGTTCACCC ACCAACTGC AAGAGGCTCA NNAAGTACTR 180
 CCAGGGTMYA SGGACMASGG TGGGAYTYCA YCACWCATCT 220

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAGGGTC TCTATCCACT GCTAAACCAT ACACCTGGGT AAACAGGGAC CATTTAACAT	60
TCCCANCTAA ATATGCCAAG TGACTTCACA TGTTTATCTT AAAGATGTCC AAAACGCAAC	120
TGATTTTCTC CCCTAAACCT GTGATGGTGG GATGATTAAN CCTGAGTGGT CTACAGCAAG	180
TTAAGTGCAA GGTGCTAAAT GAANGTGACC TGAGATACAG CATCTACAAG GCAGTACCTC	240
TCAACNCAGG GCAACTTTGC TTCTCANAGG GCATTTAGCA GTGTCTGAAG TAATTTCTGT	300
ATTACAACCTC ACGGGGCGGG GGGTGAATAT CTANTGGANA GNAGACCCTA ACG	353

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCACTGAGAG GAACTTCCAA TACYATKATC AGAGTGAACA RGCARCCYAC AGAACAGGAG	60
AAAATGTTYG CAATCTCTCC ATCTGACAAA AGGCTAATAT CCAGAWTCTA AWAGGAACTT	120
AAACAAATTT ATGAGAAAAG AACARACAAC CTCAWCAAAA AGTGGGTGAA GGAWATGCTS	180
AAARGAAGAC ATYTATTCAG CCAGTAAACA YATGAAAAAA AGGCTCATSA TCACTGAWCA	240
TTAGAGAAAT GCAAATCAAA ACCACAATGA GATACCATCT YAYRCCAGTT AGAAYGGTGA	300
TCATTAAAAAR STCAGGAAAC AACAGATGCT GGACAAGGTG TCA	343

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCACTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCCACC CTGTACTTGG GGAGAGAAAC	60
AGAAGGTGAG AAAGTCTTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT	120
TCAAAGTTCC CATGCTGCCA AAGTGCCATC CTTTGGGGTA CTGTTTTCTG AGCTCCAGTG	180
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAGTG AGCAAATCTT AAAAAGGTGG	240
CTTGAGTTCA GCCTTAAATA CCATCTTGAA ATGACACAGA GAAAGAANGA TGTGGGTGG	300
GAGTGGATAG AGACCCTAAC G	321

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCACTGAGAG	GAACTTCAGA	GAGAGAGAGA	GAGTTCCACC	CTGTACTTGG	GGAGAGAAAC	60
AGAAGGTGAG	AAAGTCTTTG	GTTCTGAAGC	AGCTTCTAAG	ATCTTTTCAT	TTGCTTCATT	120
TCAAAGTTCC	CATGCTGCCA	AAGTGCCATC	CTTTGGGGTA	CTGTTTTCTG	AGCTCCAGTG	180
ATAACTCATT	TATACAAGGG	AGATACCCAG	AAAAAAGTG	AGCAAATCTT	AAAAAGGTGG	240
CTTGAGTTCA	GYCTTAAATA	CCATCTTGAA	ATGAMACAGA	GAAAGAAGGA	TGTGGGTGG	300
GAGTGGATAG	AGACCCTAAC	G				321

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCACTGAGAG	GAACTTCCAC	ATGCACTGAG	AAATGCATGT	TCACAAGGAC	TGAAGTCTGG	60
AACTCAGTTT	CTCAGTTCCA	ATCCTGATTC	AGGTGTTTAC	CAGCTACACA	ACCTTAAGCA	120
AGTCAGATAA	CCTTAGCTTC	CTCATATGCA	AAATGAGAAT	GAAAAGTACT	CATCGCTGAA	180
TTGTTTTGAG	GATTAGAAAA	ACATCTGGCA	TGCAGTAGAA	ATTCAATTAG	TATTCATTTT	240
CATTCTTCTA	AATTAACAA	ATAGGATTTT	TAGTGGTGGA	ACTTCAGACA	CCAGAAATGG	300
GAGTGGATAG	AGACCCT					317

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGTTAGGGTC	TCTATCCACT	CCCACTACTG	ATCAAACCTCT	ATTTATTTAA	TTATTTTAT	60
CATACTTTAA	GTTCGGGAT	ACACGTGCAG	CATGCGCAGG	TTTGTTGCAT	AGGTATACAC	120
TTGCCATGGT	GGTTGCTGC	ACCCATCAGT	CCATCATCTA	CATTAGGTAT	TTCTCCTAAT	180
GCTATCCCTC	CCCTAGCCCC	TTACACCCCC	AACAGGCTCT	AGTGTGTGAA	GTTCTCTCA	240
GTGC						244

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGTTAGGGTC	TCTATCCACT	GAAATCTGAA	GCACAGGAGG	AAGAGAAGCA	GTYCTAGTGA	60
------------	------------	------------	------------	------------	------------	----

GATGGCAAGT TCWTTTACCA CACTCTTTAA CATTTYGTTT AGTTTTAACC TTTATTTATG	120
GATAATAAAG GTTAATATTA ATAATGATTT ATTTTAAGGC ATTCCCRAAT TTGCATAATT	180
CTCCTTTTGG AGATACCCTT TTATCTCCAG TGCAAGTCTG GATCAAAGTG ATASAMAGAA	240
GTTCTCTCA GTGC	254

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTTGCTC GTTTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG	240
TTCCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTCAACAGTT TCCGATGGCT GTGATGGGCA TAGTCATANT TAACNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAAGAGGGTA CCAGCAGAAA GGTTAGTATC ATCAGATAGC ATCTTATACG AGTAATATGC	60
CTGCTATTTG AAGTGTAATT GAGAAGGAAA ATTTTAGCGT GCTCACTGAC CTGCCTGTAG	120
CCCCAGTGAC AGCTAGGATG TGCATTCTCC AGCCATCAAG AGACTGAGTC AAGTTGTTCC	180
TTAAGTCAGA ACAGCAGACT CAGCTCTGAC ATTCTGATTG GAATGACACT GTTCAGGAAT	240
CGGAATCCTG TCGATTAGAC TGGACAGCTT GTGGCAAGTG AATTGCGCTG TAACAAGCCA	300
GATTTTTTAA AATTTATATT GTAAATAATG TGTGTGTGTG TGTGTGTATA TATATATATA	360
TGTACAGTTA TCTAAGTTAA TTTAAAAGTT GTTTGGTACC CTCTTA	406

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTTTTTTTTT TTTACTCGGC TCAGTCTAAT CCTTTTTGTA GTCAC TCATA GGCCAGACTT	60
AGGGCTAGGA TGATGATTAA TAAGAGGGAT GACATAACTA TTAGTGGCAG GTTAGTTGTT	120

TGTAGGGCTC ATGGTAGGGG TAAAAGGAGG GCAATTTCTA GATCAAATAA TAAGAAGGTA	180
ATAGCTACTA AGAAGAATTT TATGGAGAAA GGGACGCGGG CGGGGGATAT AGGGTCGAAAG	240
CCGCACTCGT AAGGGGTGGA TTTTCTATG TAGCCGTTGA GTTGTGGTAG TCAAAATGTA	300
ATAATTATTA GTAGTAAGCC TAGGAGA	327

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TAGTCTATGC GGTTGATTCTG GCAATCCATT ATTTGCTGGA TTTTGTCTATG TGTTTTGCCA	60
ATTGCATTCA TAATTTATTA TGCATTTATG CTTGTATCTC CTAAGTCATG GTATATAATC	120
CATGCTTTTT ATGTTTTGTC TGACATAAAC TCTTATCAGA GCCCTTTGCA CACAGGGATT	180
CAATAAATAT TAACACAGTC TACATTTATT TGGTGAATAT TGCATATCTG CTGTACTGAA	240
AGCACATTAA GTAACAAAGG CAAGTGAGAA GAATGAAAAG CACTACTCAC AACAGTTATC	300
ATGATTGCGC ATAGACTA	318

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCTTCAACCT CTAATCCAC TAATAGCTTT TTGATGACTT CTAGCAAGCC TCGCTAACCT	60
CGCCTTACCC CCCACTATTA ACCTACTGGG AGAACTCTCT GTGCTAGTAA CCACGTTCTC	120
CTGATCAAAT ATCACTCTCC TACTTACAGG ACTCAACATA CTAGTCACAG CCCTATACTC	180
CCTCTACATA TTTACCACAA CACAATGGGG CTCCTCACC CACCACATTA ACAACATAAA	240
ACCCTCATT ACACGAGAAA ACACCCTCAT GTTCATACAC CTATCCCCCA TTCTCCTCCT	300
ATCCCTCAAC CCCGACATCA TTACCGGGTT TTCCTCTT	338

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AGCCATTTAC CACCCATCCA CAAAAAAAAA AAAAAAAAAAG AAAAATATCA AGGAATAAAA	60
ATAGACTTTG AACAAAAAGG AACATTTGCT GGCCTGAGGA GGCATCACCC G	111

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCGGGTGATG CCTCCTCAGG CCAAGAAGAT AAAGCTTCAG ACCCCTAACA CATTTCCAAA	60
AAGGAAGAAA GGAGAAAAAA GGCATCATC CCCGTTCCGA AGGGTCAGGG AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG CGGACAACTC CTTTGATGCC AAGCGAGGTG CAGCCGGAGA	180
CTGGGGAGAG CGAGCCAATC AGGTTTTGAA GTTCCTCTCA GTGC	224

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCACTGAGAG GAACTTCGTT GGAAACGGGT TTTTTCATG TAAGGCTAGA CAGAAGAATT	60
CTCAGTAACT TCCTTGTTGTT GTGTGTATTC AACTCACASA GTTGAACGAT CCTTTACACA	120
GAGCAGACTT GTAACACTCT TWTTGTGGAA TTTGCAAGTG GAGATTTCAG SCGCTTTGAA	180
GTSAAAGGTA GAAAAGGAAA TATCTTCCTA TAAAACTAG ACAGAATGAT TCTCAGAAAC	240
TCCTTTGTGA TGTGTGCGTT CAACTCACAG AGTTTAACCT TTCWTTTCAT AGAAGCAGTT	300
AGGAAACACT CTGTTTGTA AGTCTGCAAG TGGATAGAGA CCCTAACG	348

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCACTGAGAG GAACTTCYTT GTGWTGKTG YATTCAACTC ACAGAGTTGA ASSWTSMTT	60
ACABAGWKCA GGCTTKCAA CACTCTTTT GTMGAATYTG CAAGWGGAKA TTTSRRCCRC	120
TTTGWGGYCW WYSKTMGAAW MGGRWATATC TTCWYATMRA AMCTAGACAG AAKSATTC	180
AKAAWSTYYY YTGTGAWGWS TGCRTTCAAC TCACAGAGKT KAACMWYCT KYTSATRGAG	240
CAGTTWKGA ACTCTMTTTC TTTGGATTCT GCAAGTGGAT AGAGACCCTA ACG	293

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTCCTAGGCT

10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTAGTTGCC

10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TTCCGTTATG C

11

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTAAAGGG

10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGGTCATAG

10

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TACAACGAGG

10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGATTGGTC

10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTTTCTACCC

10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TTTTGGCTCC

10

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGAACCAATC

10

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCGATACAGG

10

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGTACTAAGG

10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGTCTATGCG

10

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTATCCATGG

10

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGTCCACA

10

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AAGAGGGTAC

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTTCAACCTC

10

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTCCTCTTG CCTTACCAAC

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTAAGTCGAG CAGTGTGATG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTAAGTCGAG CAGTCTGATG

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GACTTAGTGG AAAGAATGTA

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTAATTCCGC CAACCGTAGT

20

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGGTTGATC GATAGTGGAA

20

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACGGGGACCC CTGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATTCTAGAC CATTGCTAC

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACATAACCAC TTTAGCGTTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGGGTGATGC CTCCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AGCATGTTGA GCCCAGACAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GACACCTTGT CCAGCATCTG

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TACGCTGCAA CACTGTGGAG

20

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGTTAGGGTC TCTATCCACT

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AGACTGACTC ATGTCCCCTA

20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCATCGCTCG GTGACTCAAG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CAAGATTCCA TAGGCTGACC

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ACGTACTGGT CTTGAAGGTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GACGCTTGGC CACTTGACAC

20

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTATCGACGT AGTGGTCTCC

20

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TAGTGACATT ACGACGCTGG

20

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGGTGATGC CTCCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGGCTATTT TCGGGGGCTG ACA

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CCGGTATCTC CTCGTGGGTA TT

22

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCCTGAGC CACAAATG

18

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CCGGAGGAGG AAGCTAGAGG AATA

24

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTTTTTTTTT TTAG

14

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser	Ser	Gly	Gly	Arg	Thr	Phe	Asp	Asp	Phe	His	Arg	Tyr	Leu	Leu	Val
1				5					10					15	
Gly	Ile														

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln	Gly	Ala	Ala	Gln	Lys	Pro	Ile	Asn	Leu	Ser	Lys	Xaa	Ile	Glu	Val
1				5					10					15	
Val	Gln	Gly	His	Asp	Glu										
				20											

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5 10 15
Thr Pro Phe Asp Leu Ser Ala
20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Tyr Leu Leu Val Gly Ile Gln Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Ala Ala Gln Lys Pro Ile Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asn Leu Ser Lys Xaa Ile Glu Val Val
1 5

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu Val Val Gln Gly His Asp Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Asn Leu Ala Phe Val Ala Gln Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Phe Val Ala Gln Ala Ala Pro Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGCGGCC	GCGAGCTCAA	TTAACCCTCA	CTAAAGGGAG	TCGACTCGAT	CAGACTGTTA	60
CTGTGTCTAT	GTAGAAAGAA	GTAGACATAA	GAGATTCCAT	TTTGTTCTGT	ACTAAGAAAA	120
ATTCTTCTGC	CTTGAGATGC	TGTTAATCTG	TAACCCTAGC	CCCAACCCTG	TGCTCACAGA	180
GACATGTGCT	GTGTTGACTC	AAGGTTCAAT	GGATTTAGGG	CTATGCTTTG	TTAAAAAAGT	240
GCTTGAAGAT	AATATGCTTG	TTAAAAGTCA	TCACCATTTCT	CTAATCTCAA	GTACCCAGGG	300
ACACAATACA	CTGCGGAAGG	CCGCAGGGAC	CTCTGTCTAG	GAAAGCCAGG	TATTGTCCAA	360
GATTTCTCCC	CATGTGATAG	CCTGAGATAT	GGCCTCATGG	GAAGGGTAAG	ACCTGACTGT	420
CCCCCAGCCC	GACATCCCCC	AGCCCCGACAT	CCCCCAGCCC	GACACCCGAA	AAGGGTCTGT	480
GCTGAGGAGG	ATTAGTAAAA	GAGGAAGGCC	TCTTTGCACT	TGAGGTAAGA	GGAAGGCATC	540
TGTCCTCCTGC	TCGTCCCTGG	GCAATAGAAT	GTCTTGGTGT	AAAACCCGAT	TGTATGTTCT	600
ACTTACTGAG	ATAGGAGAAA	ACATCCTTAG	GGCTGGAGGT	GAGACACGCT	GGCGGCAATA	660
CTGCTCTTTA	ATGCACCGAG	ATGTTTGTAT	AAGTGCACAT	CAAGGCACAG	CACCTTTCTCT	720
TAAACTTATT	TATGACACAG	AGACCTTTGT	TCACGTTTTT	CTGCTGACCC	TCTCCCCACT	780
ATTACCCCTAT	TGGCCTGCCA	CATCCCCCTC	TCCGAGATGG	TAGAGATAAT	GATCAATAAA	840
TACTGAGGGA	ACTCAGAGAC	CAGTGTCCTT	CTAGGTCCTC	CGTGTGCTGA	GCGCCGGTCC	900
CTTGGGCTCA	CTTTTCTTTC	TCTATACTTT	GTCTCTGTGT	CTCTTTCTTT	TCTCAGTCTC	960
TCGTTCCACC	TGACGAGAAA	TACCCACAGG	TGTGGAGGGG	CAGGCCACCC	CTTCAATAAT	1020
TTACTAGCCT	GTTTCGCTGAC	AACAAGACTG	GTGGTGACAG	AGGTTGGGTC	TTGGTGTTCA	1080
CCGGGTGGCA	GGCATGGGCC	AGGTGGGAGG	GTCTCCAGCG	CCTGGTGCAA	ATCTCCAAGA	1140
AAGTGCAGGA	AACAGCACCA	AGGTGATTG	TAAATTTTGA	TTTGGCGCGG	CAGGTAGCCA	1200
TTCCAGCGCA	AAAATGCGCA	GGAAAGCTTT	TGCTGTGCTT	GTAGGCAGGT	AGGCCCAAG	1260
CACCTCTTAT	TGGCTAATGT	GGAGGGAACC	TGCACATCCA	TTGGCTGAAA	TCTCCGTCTA	1320
TTTGAGGCTG	ACTGAGCGCG	TTCTTTCTTT	CTGTGTTGCC	TGGAACGGA	CTGTCTGCCT	1380
AGTAACATCT	GATCACGTTT	CCCATTGGCC	GCCGTTTCCG	GAAGCCCGCC	CTCCCATTTC	1440
CGGAAGCCTG	GCGCAAGGTT	GGTCTGCAGG	TGGCCTCCAG	GTGCAAAGTG	GGAAGTGTGA	1500
GTCTCAGTC	TTGGGCTATT	CGGCCACGTG	CCTGCCGGAC	ATGGGACGCT	GGAGGGTCAG	1560
CAGCGTGAG	TCCTGGCCTT	TTGCGTCCAC	GGGTGGGAAA	TTGGCCATTG	CCACGGCGGG	1620
AAGTGGGACT	CAGGCTGCCC	CCCGGCCGTT	TCTCATCCGT	CCACCGGACT	CGTGGGCGCT	1680
CGCACTGGCG	CTGATGTAGT	TTCTTGACCT	CTGACCCGTA	TTGTCTCCAG	ATTAAAGGTA	1740
AAAACGGGGC	TTTTTCAGCC	CACTCGGTA	AAACGCCTTT	TGATTTCTAG	GCAGGTGTTT	1800
TGTTGCACGC	CTGGGAGGGA	GTGACCCGCA	GGTTGAGGTT	TATTAAAATA	CATTCCTGGT	1860
TTATGTTATG	TTTATAATAA	AGCACCCCAA	CCTTTACAAA	ATCTCACTTT	TTGCCAGTTG	1920
TATTATTTAG	TGGACTGTCT	CTGATAAGGA	CAGCCAGTTA	AAATGGAATT	TTGTTGTTGC	1980
TAATTAAACC	AATTTTTAGT	TTTGGTGTTT	GTCTTAATAG	CAACAACCTC	TCAGGCTTTA	2040
TAAAACCATA	TTTCTTGGGG	GAAATTTCTG	TGTAAGGCAC	AGCGAGTTAG	TTTGGGAATTG	2100
TTTTAAAGGA	AGTAAGTTCC	TGGTTTTGAT	ATCTTAGTAG	TGTAATGCCC	AACCTGGTTT	2160
TTACTAACCC	TGTTTTTAGA	CTCTCCCTTT	CCTTAAATCA	CCTAGCCTTG	TTTCCACCTG	2220
AATTGACTCT	CCCTTAGCTA	AGAGCGCCAG	ATGGACTCCA	TCTTGGCTCT	TTCCTGGCA	2280
GCCCCCTCCT	CAAGGACTTA	ACTTGTGCAA	GCTGACTCCC	AGCACATCCA	AGAATGCAAT	2340
TAACTGTTAA	GATACTGTGG	CAAGCTATAT	CCGCAGTTCC	GAGGAATTCA	TCCGATTGAT	2400
TATGCCCAAA	AGCCCCGCGT	CTATCACCTT	GTAATAATCT	TAAAGCCCCT	GCACCTGGAA	2460
CTATTAACTT	TCCTGTAACC	ATTTATCCTT	TTAACTTTTT	TGCTTACTTT	ATTTCTGTAA	2520
AATTGTTTTA	ACTAGACCTC	CCCTCCCCTT	TCTAAACCAA	AGTATAAAAG	AAGATCTAGC	2580
CCCTTCTTCA	GAGCGGAGAG	AATTTTGAGC	ATTAGCCATC	TCTTGGCGGC	CAGCTAAATA	2640
AATGGACTTT	TAATTTGTCT	CAAAGTGTGG	CGTTTTCTCT	AACTCGCTCA	GGTACGACAT	2700

TTGGAGGCCC	CAGCGAGAAA	CGTCACCGGG	AGAAACGTCA	CCGGGCGAGA	GCCGGGCCCCG	2760
CTGTGTGCTC	CCCCGGAAGG	ACAGCCAGCT	TGTAGGGGGG	AGTGCCACCT	GAAAAAAAAAA	2820
TTTCCAGGTC	CCCAAAGGGT	GACCGTCTTC	CGGAGGACAG	CGGATCGACT	ACCATGCGGG	2880
TGCCCCACAA	AATTCCACCT	CTGAGTCCTC	AACTGCTGAC	CCCGGGGTCA	GGTAGGTCAG	2940
ATTTGACTTT	GGTTCTGGCA	GAGGGAAGCG	ACCCTGATGA	GGGTGTCCCT	CTTTTGA CTC	3000
TGCCCCATTT	TCTAGGATGC	TAGAGGGTAG	AGCCCTGGTT	TTCTGTTAGA	CGCCTCTGTG	3060
TCTCTGTCTG	GGAGGGAAGT	GGCCCTGACA	GGGGCCATCC	CTTGAGTCAG	TCCACATCCC	3120
AGGATGCTGG	GGGACTGAGT	CCTGGTTTCT	GGCAGACTGG	TCTCTCTCTC	TCTCTTTTTT	3180
TATCTCTAAT	CTTTCCTTGT	TCAGGTTTCT	TGGAGAATCT	CTGGGAAAGA	AAAAAGAAAA	3240
ACTGTTATAA	ACTCTGTGTG	AATGGTGAAT	GAATGGGGGA	GGACAAGGGC	TTGCGCTTGT	3300
CCTCCAGTTT	GTAGCTCCAC	GGCGAAAGCT	ACGGAGTTCA	AGTGGGCCCT	CACCTGCGGT	3360
TCCGTGGCGA	CCTCATAAGG	CTTAAGGCAG	CATCCGGCAT	AGCTCGATCC	GAGCCGGGGG	3420
TTTATACCGG	CCTGTCAATG	CTAAGAGGAG	CCCAAGTCCC	CTAAGGGGGA	GCGGCCAGGC	3480
GGGCATCTGA	CTGATCCCAT	CACGGGACCC	CCTCCCTTG	TTTGTCTAAA	AAAAAAAAAAA	3540
GAAGAACTG	TCATAACTGT	TTACATGCCC	TAGGGTCAAC	TGTTTGT TTT	ATGTTTATTG	3600
TTCTGTTCCG	TGTCTATTGT	CTTGTTTAGT	GGTTGTCAAG	GTTTTGCATG	TCAGGACGTC	3660
GATATTGCCC	AAGACGTCTG	GGTAAGAACT	TCTGCAAGGT	CCTTAGTGCT	GATTTTTTGT	3720
CACAGGAGGT	TAAATTTCTC	ATCAATCATT	TAGGCTGGCC	ACCACAGTCC	TGTCTTTTCT	3780
GCCAGAAGCA	AGTCAGGTGT	TGTTACGGGA	ATGAGTGTA	AAAAACATTC	GCCTGATTGG	3840
GATTTCTGGC	ACCATTGATG	TTGTATTTAG	ATTGTCATAC	CCCACATCCA	GGTTGATTGG	3900
ACCTCCTCTA	AACTAAACTG	GTGGTGGGTT	CAAAACAGCC	ACCCTGCAGA	TTTCCTTGCT	3960
CACCTCTTTG	GTCATTCTGT	AACTTTTCTC	GTGCCCTTAA	ATAGCACACT	GTGTAGGGAA	4020
ACCTACCCTC	GTA CTGCTTT	ACTTCGTTTA	GATTCCTTACT	CTGTTCTCTC	GTGGCTACTC	4080
TCCCATCTTA	AAAACGATCC	AAGTGGTCTC	TTTCCTCCTC	CCTGCCCCCT	ACCCACACA	4140
TCTCGTTTTT	CAGTGCGACA	GCAAGTTCAG	CGTCTCCAGG	ACTTGGCTCT	GCTCTCACTC	4200
CTTGAACCCT	TAAAAGAAAA	AGCTGGGTTT	GAGCTATTTG	CCTTTGAGTC	ATGGAGACAC	4260
AAAAGGTATT	TAGGGTACAG	ATCTAGAAGA	AGAGAGAGAA	CACCTAGATC	CAACTGACCC	4320
AGGAGATCTC	GGGCTGGCCT	CTAGTCCTCC	TCCCTCAATC	TAAAGCTAC	AGTGATGTGG	4380
CAAGTGGTAT	TTAGCTGTTG	TGGTTTTTCT	GCTCTTTCTG	GTCATGTTGA	TTCTGTTCTT	4440
TGCATACTCC	AGCCCCCAG	GGAGTGAGTT	TCTCTGTCTG	TGCTGGGTTT	GATATCTATG	4500
TTCAAATCTT	ATTAAATTGC	CTTCAAAAAA	AAAAAAAAAA	GGGAAACACT	TCCTCCAGC	4560
CTTGTAAGGG	TTGGAGCCCT	CTCCAGTATA	TGCTGCAGAA	TTTTTCTCTC	GGTTTCTCAG	4620
AGGATTATGG	AGTCCGCTT	AAAAAAGGCA	AGCTCTGGAC	ACTCTGCAAA	GTA GAATGGC	4680
CAAAGTTTGG	AGTTGAGTGG	CCCCTTGAAG	GGTCACTGAA	CCTCACAATT	GTTCAAGCTG	4740
TGTGGCGGGT	TGTTACTGAA	ACTCCCGGCC	TCCCTGATCA	GTTTCCCTAC	ATTGATCAAT	4800
GGCTGAGTTT	GGTCAGGAGC	ACCCCTTCCA	TGGCTCCACT	CATGCACCAT	TCATAATTTT	4860
ACCTCCAAGG	TCCCTCTGAG	CCAGACCGTG	TTTTCGCCTC	GACCCTCAGC	CGGTTTCAGCT	4920
CGCCCTGTAC	TGCCCTCTCT	TGAAGAAGAG	GAGAGTCTCC	CTCACCCAGT	CCCACCGCCT	4980
TAAAACCAGC	CTACTCCCTT	AGGGTCAATC	CATGTCTCCT	CGGCTATGTC	CCCTGTAGGC	5040
TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	TGGTGGGAGG	AAGTAGCCCC	TCTACTACCA	5100
CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	CCCCCTTCTC	GGTTTATGTC	5160
CCTTCTTTCT	ACTTCTGACT	TGTATAATTG	GAAAACCCAT	AATCCTCCCT	TCTCTGAAAA	5220
GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	ACACATTGGC	CCACCTGGGA	5280
TGACTGTCAA	CAGCTCCTTT	TGACCCTTTT	CACCTCTGAA	GAGAGGGAAA	GTATCCAAAG	5340
AGAGGCCAAA	AAGTACAACC	TCACATCAAC	CAATAGGCCG	GAGGAGGAAG	CTAGAGGAAT	5400
AGTGATTAGA	GACCCAATTG	GGACCTAATT	GGGACCCAAA	TTTCTCAAGT	GGAGGGAGAA	5460
CTTTTGACGA	TTTCCACCGG	TATCTCCTCG	TGGGTATTCA	GGGAGCTGCT	CAGAAACCTA	5520
TAAACTTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	TGAGTCACCA	GGAGTGTTTT	5580
TAGAGCACCT	CCAGGAGGCT	TATCGGATTT	ACACCCCTTT	TGACCTGGCA	GCCCCGAAA	5640
ATAGCCATGC	TCTTAATTTG	GCATTTGTGG	CTCAGGCAGC	CCCAGATAGT	AAAAGGAAAC	5700
TCCAAAAACT	AGAGGGATTT	TGCTGGAATG	AATACCAGTC	AGCTTTTAGA	GATAGCCTAA	5760
AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAAACAAG	CAGCTCAGGC	AGCTGAAAAA	5820
AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	TAGATCAGCC	TCATTTGACT	5880
TCCCTCCCA	TATGGTGTTT	AAATCCAGCT	ACACTACTTC	CTGACTCAA	CTCCACTATT	5940
CCTGTTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	CTGGCCGACC	TGATCTTCAA	6000

AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	GTGTTCACAG	ACAGTAGCAG	CTTCCTCGAG	6060
AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	CAGATGTGTT	GTGGGCTCAG	6120
GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	TCGCCCTCAC	TCAGGCTCTC	6180
CGATGGGGTA	AGGATATTAA	CGTTAACT	GACAGCAGGT	ACGCCTTTGC	TACTGTGCAT	6240
GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	CAGCAGGTGG	CTGTAATCCA	6300
CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCCG	GGTAACCAGA	AAGCTGATTC	6360
AGCAGCTCAA	GATGCAGTGT	GACTTTTCAGT	CACGCCTCTA	AACTTGCTGC	CCACAGTCTC	6420
CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	ACAGAAGAAG	AAAAGTGGCC	6480
TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	TTCTTCCTGA	CTCTAGAATC	6540
TTCATACCCC	GAACCTTTGG	GAAAACCTTTA	ATCAGTCACC	TACAGTCTAC	CACCCATTTA	6600
GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	AGATCCCCCA	TCTTCAAAGC	6660
CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	CAAAAAAGGT	6720
CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACCTCAC	CAGGAGAAAA	GTGGGAAATT	6780
GACTTTACAG	AAGTAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	ACTGGTAGAC	6840
ACCTTCTCTG	GATGGACTGA	AGCATTGTCT	ACCAAAAACG	AAACTGTCAA	TATGGTAGTT	6900
AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	AGGGTCTGAT	6960
AATGGACCGG	CCTTCGCCTT	GTCTATAGTT	TAGTCAGTCA	GTAAGGCGTT	AAACATTCAA	7020
TGGAAGCTCC	ATTGTGCCTA	TCGACCCAG	AGCTCTGGGC	AAGTAGAACG	CATGAAGTGC	7080
ACCCTAACAAA	ACACTCTTAC	AAAATTAATC	TTAGAAACCG	GTGTAAATTG	TGTAAGTCTC	7140
CTTCCTTTAG	CCCTACTTAG	AGTAAGGTGC	ACCCCTTACT	GGGCTGGGTT	CTTACCTTTT	7200
GAAATCATGT	ATGGGAGGGC	GCTGCCTATC	TTGCCTAAGC	TAAGAGATGC	CCAATTGGCA	7260
AAAATATCAC	AACTAATTT	ATTACAGTAC	CTACAGTCTC	CCCAACAGGT	ACAAGATATC	7320
ATCCTGCCAC	TTGTTTCGAGG	AACCCATCCC	AATCCAATTC	CTGAACAGAC	AGGGCCCTGC	7380
CATTCATTCC	CGCCAGGTGA	CCTGTTGTTT	GTAAAAAGT	TCCAGAGAGA	AGGACTCCCT	7440
CCTGCTTGGA	AGAGACCTCA	CACCGTCATC	ACGATGCCAA	CGGCTCTGAA	GGTGGATGGC	7500
ATTCCTGCGT	GGATTTCATCA	CTCCCGCATC	AAAAAGGCCA	ACGGAGCCCA	ACTAGAAACA	7560
TGGGTCCCCA	GGGCTGGGTC	AGGCCCTTTA	AAACTGCACC	TAAGTTGGGT	GAAGCCATTA	7620
GATTAATTCT	TTTTCTTAAT	TTTGTAACAC	AATGCATAGC	TTCTGTCAAA	CTTATGTATC	7680
TTAAGACTCA	ATATAACCCC	CTTGTTATAA	CTGAGGAATC	AATGATTTGA	TTCCCCAAAA	7740
ACACAAGTGG	GGAATGTAGT	GTCCAACCTG	GTTTTTACTA	ACCCTGTTTT	TAGACTCTCC	7800
CTTTCCTTTA	ATCACTCAGC	CTTGTTTCCA	CCTGAATTGA	CTCTCCCTTA	GCTAAGAGCG	7860
CCAGATGGAC	TCCATCTTGG	CTCTTTTCACT	GGCAGCCGCT	TCCTCAAGGA	CTTAAGTGT	7920
GCAAGCTGAC	TCCCAGCACA	TCCAAGAATG	CAATTAAGT	ATAAGATACT	GTGGCAAGCT	7980
ATATCCGCAG	TTCCCAGGAA	TTCGTCCAAT	TGATTACACC	CAAAAGCCCC	GCGTCTATCA	8040
CCTTGTAATA	ATCTTAAAGC	CCCTGCACCT	GGAAGTATTA	ACGTTCCCTGT	AACCATTTAT	8100
CCTTTTAACT	TTTTTGCCCTA	CTTTATTTCT	GTAAATTTGT	TTTAACTAGA	CCCCCCTCT	8160
CCTTTCTAAA	CCAAAGTATA	AAAGCAAATC	TAGCCCTTTC	TTCAGGCCGA	GAGAATTTTCG	8220
AGCGTTAGCC	GTCTCTTGGC	CACCAGCTAA	ATAAACGGAT	TCTTCATGTG	TCTCAAAGTG	8280
TGGCGTTTTT	TCTAACTCGC	TCAGGTACGA	CCGTGGTAGT	ATTTTCCCCA	ACGTCTTATT	8340
TTTAGGGCAC	GTATGTAGAG	TAAGTTTTAT	GAAAGAAACC	AGTTAAGGAG	GTTTTGGGAT	8400
TTCCTTTATC	AACTGTAATA	CTGGTTTTGA	TTATTTATTT	ATTTATTTAT	TTTTTTTGAG	8460
AAGGAGTTTC	ACTCTTGTTG	CCCAGGCTGG	AGTGCAATGG	TGCGATCTTG	GCTCACTGCA	8520
ACTTCCGCCT	CCCAGGTTCA	AGCGATTCTC	CTGCCTCAGC	CTCGAGAGTA	GCTGGGATTA	8580
TAGGCATGCG	CCACCACACC	CAGCTAATTT	TGTATTTTTA	GTAAAGATGG	GGTTTCTTCA	8640
TGTTGGTCAA	GCTGGTCTGG	AACTCCCCGC	CTCGGGTGAT	CTGCCCCGCT	CGGCCTCCGA	8700
AAGTGCTGGG	ATTACAGGTG	TGATCCACCA	CACCCAGCCG	ATTTATATGT	ATATAAATCA	8760
CATTCCTCTA	ACCAAAATGT	AGTGTTCCT	TCCATCTTGA	ATATAGGCTG	TAGACCCCGT	8820
GGGTATGGGA	CATTGTTAAC	AGTGAGACCA	CAGCAGTTTT	TATGTCATCT	GACAGCATCT	8880
CCAAATAGCC	TTCATGGTTG	TCACTGCTTC	CCAAGACAAT	TCCAAATAAC	ACTTCCCAGT	8940
GATGACTTGC	TACTTGCTAT	TGTTACTTAA	TGTGTTAAGG	TGGCTGTTAC	AGACACTATT	9000
AGTATGTCAG	GAATTACACC	AAAATTTAGT	GGCTCAAACA	ATCATTTTAT	TATGTATGTG	9060
GATTCTCATG	GTCAGGTCAG	GATTTTCAGAC	AGGGCACAAG	GGTAGCCAC	TTGTCTCTGT	9120
CTATGATGTC	TGGCCTCAGC	ACAGGAGACT	CAACAGCTGG	GGTCTGGGAC	CATTTGGAGG	9180
CTTGTTCCCT	CACATCTGAT	ACCTGGCTTG	GGATGTTGGA	AGAGGGGGTG	AGCTGAGACT	9240
GAGTGCCTAT	ATGTAGTGTT	TCCATATGGC	CTTGACTTCC	TTACAGCCTG	GCAGCCTCAG	9300

GGTAGTCAGA ATTCTTAGGA GGCACAGGGC TCCAGGGCAG ATGCTGAGGG GTCTTTTATG 9360
 AGGTAGCACA GCAAATCCAC CCAGGATC 9388

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TGTAAGTCGA GCAGTGTGAT GGAAGGAATG GTCTTTGGAG AGAGCATATC CATCTCCTCC	60
TCACTGCCTC CTAATGTCAT GAGGTACACT GAGCAGAATT AAACAGGGTA GTCTTAACCA	120
CACTATTTTT AGCTACCTTG TCAAGCTAAT GGTAAAGAA CACTTTTGGT TTACACTTGT	180
TGGGTCATAG AAGTTGCTTT CCGCCATCAC GCAATAAGTT TGTGTGTAAT CAGAAGGAGT	240
TACCTTATGG TTTCAGTGTC ATTCTTTAGT TAAGTTGGGA GCTGTGTAAT TTAGGCTTTG	300
CGTATTATTT CACTTCTGTT CTCCACTTAT GAAGTGATTG TGTGTTCCGG TGTGTGTGCG	360
TGCGCATGTG CTTCCGGCAG TTAACATAAG CAAATACCCA ACATCACACT GCTCGACTT	419

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGTAAGTCGA GCAGTGTGAT GTCCACTGCA GTGTGTTGCT GGGAACAGTT AATGAGCAAA	60
TTGTATACAA TGGCTAGTAC ATTGACCGGG ATTTGTTGAA GCTGGTGAGT GTTATGACTT	120
AGCCTGTTAG ACTAGTCTAT GCACATGGCT CTGGTCAACT ACCGCTCTCT CATTCTCTCA	180
GATAAATCCC CCATGCTTTA TATTCTCTTC CAAACATACT ATCCTCATCA CCACATAGTT	240
CCTTTGTTAA TGCTTTGTTT TAGACTTTCC CTTTTCTGTT TTCTTATTCA AACCTATATC	300
TCTTTGCATA GATTGTAAAT TCAAATGCCC TCAGGGTGCA GGCAGTTCAT GTAAGGGAGG	360
GAGGCTAGCC AGTGAGATCT GCATCACACT GCTCGACTTA CA	402

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TCGGGTGATG CCTCCTCAGG CCAAGAAGAT AAAGCTTCAG ACCCCTAACA CATTTCCAAA	60
AAGGAAGAAA GGAGAAAAA GGGCATCATC CCCGTTCCGA AGGGTCAGGG AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG CGGACAACCT CTTTGATGCC AAGCGAGGTG CAGCCGGAGA	180

CTGGGGAGAG CGAGCCAATC AGGTTTTGAA GTTCCTCTCA GTGC

224

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCCATTTAC CACCCATCCA CAAAAAAAAA AAAAAAAAAAG AAAAAATATCA AGGAATAAAA	60
ATAGACTTTG AACAAAAAGG AACATTTGCT GGCCTGAGGA GGCATCACCC G	111

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TAGCATGTTG AGCCCAGACA CTTGTAGAGA GAGGAGGACA GTTAGAAGAA GAAGAAAAGT	60
TTTTAAATGC TGAAAGTTAC TATAAGAAAG CTTTGGCTTT GGATGAGACT TTAAAGATG	120
CAGAGGATGC TTTGCAGAAA CTTCATAAAT ATATGCAGGT GATTCCTTAT TTCCTCCTAG	180
AAATTTAGTG ATATTTGAAA TAATGCCCAA ACTTAATTTT CTCCTGAGGA AAACATTTCT	240
ACATTACTTA AGTAAGGCAT TATGAAAAGT TTCTTTTGTAG GTATAGTTTT TCCTAATTGG	300
GTTTGACATT GCTTCATAGT GCCTCTGTTT TTGTCCATAA TCGAAAGTAA AGATAGCTGT	360
GAGAAACTA TTACCTAAAT TTGGTATGTT GTTTTGAGAA ATGTCCTTAT AGGGAGCTCA	420
CCTGGTGGTT TTAAATTAT TGTGCTACT ATAATTGAGC TAATTATAAA AACCTTTTGT	480
AGACATATTT TAAATTGTCT TTTCCTGTAA TACTGATGAT GATGTTTTCT CATGCATTTT	540
CTTCTGAATT GGGACCATG CTGCTGTGTC TGGGCTCACA TGCTA	585

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TAGCATGTTG AGCCCAGACA CTGGGCAGCG GGGGTGGCCA CGGCAGCTCC TGCCGAGCCC	60
AAGCGTGTTC GTCTGTGAAG GACCCTGACG TCACCTGCCA GGCTAGGGAG GGGTCAATGT	120
GGAGTGAATG TTCACCGACT TTCGCAGGAG TGTGCAGAAG CCAGGTGCAA CTTGGTTTTGC	180
TTGTGTTTCAT CACCCCTCAA GATATGCACA CTGCTTTCCA AATAAAGCAT CAACTGTCAT	240
CTCCAGATGG GGAAGACTTT TTCTCCAACC AGCAGGCAGG TCCCCATCCA CTCAGACACC	300
AGCACGTCCA CCTTCTCGGG CAGCACCACG TCCTCCACCT TCTGCTGGTA CACGGTGATG	360

ATGTCAGCAA AGCCGTTCTG CANGACCAGC TGCCCCGTGT GCTGTGCCAT CTCACTGGCC	420
TCCACCGCGT ACACCGCTCT AGGCCGCGCA TANTGTGCAC AGAANAAATG ATGATCCAGT	480
CCCACAGCCC ACGTCCAAGA NGACTTTATC CGTCAGGGAT TCTTTATTCT GCAGGATGAC	540
CTGTGGTATT AATTGTTTCGT GTCTGGGCTC AACATGCTA	579

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGACACCTTG TCCAGCATCT GCAAGCCAGG AAGAGAGTCC TCACCAAGAT CCCCACCCCG	60
TTGGCACCAG GATCTTGGAC TTCCAATCTC CAGAACTGTG AGAAATAAGT ATTTGTGCT	120
AAATAAATCT TTGTGGTTTC AGATATTTAG CTATAGCAGA TCAGGCTGAC TAAGAGAAAC	180
CCCATAAGAG TTACATACTC ATTAATCTCC GTCTCTATCC CCAGGTCTCA GATGCTGGAC	240
AAGGTGTCA	249

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGACACCTTG TCCAGCATCT GCTATTTTGT GACTTTTTTAA TAATAGCCAT TCTGACTGGT	60
GTGAGATGGT AACTCATTGT GGGTTTGGTC TGCATTTCTC TAATGATCAG TGATATTAAG	120
CTTTTTTTAA ATATGCTTGT TGACCACATG TATATCATCT TTTGAGAAGT GTCTGTTTCAT	180
ATCCTTTGCC CACTTTTTTAA TTTTATTC TTGTAAATTT GTTTAATTC CTTACAGATG	240
CTGGACAAGG TGTC	255

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTACGCTGCA AACTGTGGA GGCCAAGCTG GGATCACTTC TTCATTCTAA CTGGAGAGGA	60
GGGAAGTTCA AGTCCAGCAG AGGGTGGGTG GGTAGACAGT GGCCTCAGA AATGTCAGCT	120
GGACCCCTGT CCCCAGCATG GCAGGACAGC AAGGCTGTGG CTCTCCAGGG CCAGCTGAAG	180
AACAGGACAC TGTCTCCGCT GCCACAAAGC GTCAGAGACT CCCATCTTTG AAGCACGGCC	240
TTCTTGGTCT TCCTGCACTT CCCTGTTCTG TTAGAGACCT GGTATAGAC AAGGCTTCTC	300

CACAGTGTTG CAGCGTAA

318

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TNACGCNGCN	ACNNTGTAGA	GANGGNAAGG	CNTTCCCCAC	ATTNCCCCTT	CATNANAGAA	60
TTATTCNACC	AAGNNTGACC	NATGCCNTTT	ATGACTTACA	TGCNNACTNC	NTAATCTGTN	120
TCNNGCCTTA	AAAGCNNNTC	CACTACATGC	NTCANCACTG	TNTGTGTNAC	NTCATNAACT	180
GTCNGNAATA	GGGGCNCATA	ACTACAGAAA	TGCANTTCAT	ACTGCTTCCA	NTGCCATCNG	240
CGTGTGGCCT	TNCCTACTCT	TCTTNTATT	CAAGTAGCAT	CTCTGGANTG	CTTCCCCACT	300
CTCCACATTG	TTGCAGCNAT	AAT				323

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TCAAGATTCC	ATAGGCTGAC	CAGTCCAAGG	AGAGTTGAAA	TCATGAAGGA	GAGTCTATCT	60
GGAGAGAGCT	GTAGTTTTGA	GGGTTGCAAA	GACTTAGGAT	GGAGTTGGTG	GGTGTGGTTA	120
GTCTCTAAGG	TTGATTTTGT	TCATAAATTT	CATGCCCTGA	ATGCCTTGCT	TGCCTCACCC	180
TGGTCCAAGC	CTTAGTGAAC	ACCTAAAAGT	CTCTGTCTTC	TTGCTCTCCA	AACTTCTCCT	240
GAGGATTTCC	TCAGATTGTC	TACATTGAGA	TGAAGCCAG	TTGGCAAACA	AGATGCAGTC	300
CAGAGGGTCA	G					311

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CAAGATTCCA	TAGGCTGACC	AGGAGGCTAT	TCAAGATCTC	TGGCAGTTGA	GGAAGTCTCT	60
TTAAGAAAAT	AGTTTAAACA	ATTTGTAA	ATTTTCTGT	CTTACTTCAT	TTCTGTAGCA	120
GTTGATATCT	GGCTGTCCTT	TTTATAATGC	AGAGTGGGAA	CTTCCCTAC	CATGTTTGAT	180
AAATGTTGTC	CAGGCTCCAT	TGCCAATAAT	GTGTTGTCCA	AAATGCCTGT	TTAGTTTTTA	240
AAGACGGAAC	TCCACCCTTT	GCTTGGTCTT	AAGTATGTAT	GGAATGTTAT	GATAGGACAT	300
AGTAGTAGCG	GTGGTCAGCC	TATGGAATCT	TG			332

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TCAAGATTCC ATAGGCTGAC CTGGACAGAG ATCTCCTGGG TCTGGCCCAG GACAGCAGGC	60
TCAAGCTCAG TGGAGAAGGT TTCCATGACC CTCAGATTCC CCCAAACCTT GGATTGGGTG	120
ACATTGCATC TCCTCAGAGA GGGAGGAGAT GTANGTCTGG GCTTCCACAG GGACCTGGTA	180
TTTTAGGATC AGGGTACCGC TGGCCTGAGG CTGGATCAT TCANAGCCTG GGGGTGGAAT	240
GGCTGGCAGC CTGTGGCCCC ATTGAAATAG GCTCTGGGGC ACTCCCTCTG TTCCTANTTG	300
AACTTGGGTA AGGAACAGGA ATGTGGTCAN CCTATGGAAT CTGA	345

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GACGCTTGGC CACTTGACAC ATTAAACAGT TTTGCATAAT CACTANCATG TATTTCTAGT	60
TTGCTGTCTG CTGTGATGCC CTGCCCTGAT TCTCTGGCGT TAATGATGGC AAGCATAATC	120
AAACGCTGTT CTGTTAATTC CAAGTTATAA CTGGCATTGA TTAAAGCATT ATCTTTCACA	180
ACTAAACTGT TCTTCATANA ACAGCCATA TTATTATCAA ATTAAGAGAC AATGTATTCC	240
AATATCCTTT ANGGCCAATA TATTTNATGT CCCTTAATTA AGAGCTACTG TCCGT	295

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GACGCTTGGC CACTTGACAC TGCAGTGGGA AAACCAGCAT GAGCCGCTGC CCCCAGGAA	60
CCTCGAAGCC CAGGCAGAGG ACCAGCCATC CCAGCCTGCA GGTAAAGTGT GTCACCTGTC	120
AGGTGGGCTT GGGGTGAGTG GGTGGGGGAA GTGTGTGTGC AAAGGGGGTG TNAATGTNTA	180
TGCGTGTGAG CATGAGTGAT GGCTAGTGTG ACTGCATGTC AGGGAGTGTG AACAAGCGTG	240
CGGGGGTGTG TGTGCAAGTG CGTATGCATA TGAGAATATG TGTCTGTGGA TGAGTGCAAT	300
TGAAAGTCTG TGTGTGTGCG TGTGGTCATG ANGGTAANTT ANTGACTGCG CAGGATGTGT	360
GAGTGTGCAT GGAACACTCA NTGTGTGTGT CAAGTGGCCN ANCGTC	406

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TGACGCTTGG CCACTTGACA CACTAAAGGG TGTTACTCAT CACTTTCTTC TCTCCTCGGT	60
GGCATGTGAG TGCATCTATT CACTTGGCAC TCATTTGTTT GGCAGTGACT GTAANCCANA	120
TCTGATGCAT ACACCAGCTT GTAAATTGAA TAAATGTCTC TAATACTATG TGCTCACAAT	180
ANGGTANGGG TGAGGAGAAG GGGAGAGA	208

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTCAACCTC CTTCAACCTC CTTCAACCTC CTGGATTCAA ACAATCATCC CACCTCAGAC	60
TCCTTAGTAG CTGAGACTAC AGACTCACGC CACTACATCT GGCTAAATTT TTGTAGAGAT	120
AGGGTTTCAT CATGTTGCCC TGGCTGGTCT CAAACTCCTG ACCTCAAGCA ATGTGCCAC	180
CTCAGCCTCC CAAAGTGCTG GGATTACAGG CATAAGCCAC CATGCCCACT CCATNTTTAA	240
TCTTTCCTAC CACATTCTTA CCACACTTTC TTTTATGTTT AGATACATAA ATGCTTACCA	300
TTATGATACA ATTGCCCACA GTATTAAGAC AGTAACATGC TGCACAGGTT TGTAGCCTAG	360
GAACAGTAGG CAATACCACA TAGCTTAGGT GTGTGGTAGA CTATACCATC TAGGTTTGTG	420
TAAGTTACAC TTTATGCTGT TTACACAATG ACAAACCCTA CTAATGATGC ATTTCTCAGA	480
ATGTATCCTT GTCAGTAAGC TATGATGTAC AGGGAACACT GCCCAAGGAC ACAGATATTG	540
TACCTGT	547

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GCTCCTCTTG CTTACCAAC TCACCCAGTA TGTCAGCAAT TTTATCRGCT TTACCTACGA	60
AACAGCCTGT ATCCAAACAC TTAACACACT CACCTGAAAA GTTCAGGCAA CAATCGCCTT	120
CTCATGGGTC TCTCTGCTCC AGTTCTGAAC CTTTCTCTTT TCCTAGAACA TGCATTTARG	180
TCGATAGAAG TTCCTCTCAG TGC	203

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

TGTAAGTCGA GCAGTGTGAT GGGTGGAACA GGGTTGTAAG CAGTAATTGC AAACGTGATT      60
TAAACAATAA TAATAATATT TAGCATTTAT AGAGCACTTT ATATCTTCAA AGTACTTGCA      120
AACATTAYCT AATTAAATAC CCTCTCTGAT TATAATCTGG ATACAAATGC ACTTAAACTC      180
AGGACAGGGT CATGAGARAA GTATGCATTT GAAAGTTGGT GCTAGCTATG CTTTAAAAAC      240
CTATACAATG ATGGGAAAGT TAGAGTTCAG ATTCTGTTGG ACTGTTTTTG TGCATTTTCAG      300
TTCAGCCTGA TGGCAGAATT AGATCATATC TGCACTCGAT GACTYTGCTT GATAACTTAT      360
CACTGAAATC TGAGTGTGTA TCATCACACT GCTCGACTTA CA                          402

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(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

AGCATGTTGA GCCCAGACAC TGACCAGGAG AAAAACCAAC CAATAGAAAC ACGCCCAGAC      60
ACTGACCAGG AGAAAAACCA ACCAATAAAA ACAGGCCCGG ACATAAGACA AATAATAAAA      120
TTAGCGGACA AGGACATGAA AACAGCTATT GTAAGAGCGG ATATAGTGGT GTGTGTCTGG      180
GCTCAACATG CTA                          193

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

TGTTGAGCCC AGACACTGAC CAGGAGAAAA ACCAACCAAT AAAAACAGGC CCGGACATAA      60
GACAAATAAT AAAATTAGCG GACAAGGACA TGAAAACAGC TATTGTAAGA GCGGATATAG      120
TGTTGTGTGT CTGGGCTCAA CATGCTA                          147

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

TAGCATGTTG	AGCCAGACA	CAAATCTTTC	CTTAAGCAAT	AAATCATTTTC	TGCATATGTT	60
TTTAAACCA	CAGCTAAGCC	ATGATTATTC	AAAAGGACTA	TTGTATTGGG	TATTTTGATT	120
TGGGTTCTTA	TCTCCCTCAC	ATTATCTTCA	TTTCTATCAT	TGACCTCTTA	TCCCAGAGAC	180
TCTCAAACCTT	TTATGTTATA	CAAATCACAT	TCTGTCTCAA	AAAATATCTC	ACCCACTTCT	240
CTTCTGTTTC	TGCGTGTGTA	TGTGTGTGTG	TGTGTGTCTG	GGCTCAACAT	GCTA	294

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CGGGATTGGC	TTTGAGCTGC	AGATGCTGCC	TGTGACCGCA	CCCGGCGTGG	AACAGAAAGC	60
CACCTGGCTG	CAAGTGCGCC	AGAGCCGCCC	TGACTACGTG	CTGCTGTGGG	GCTGGGGCGT	120
GATGAACCTC	ACCGCCCTGA	AGGAAGCCCA	GGCCACCGGA	TACCCCGCG	ACAAGATGTA	180
CGGCGTGTGG	TGGGCCGGTG	CGGAGCCCGA	TGTGCGTGAC	GTGGGCGAAG	GCGCCAAGGG	240
CTACAACGCG	CTGGCTCTGA	ACGGCTACGG	CACGCAGTCC	AAGGTGATCC	ANGACATCCT	300
GAAACACGTG	CACGACAAGG	GCCAGGGCAC	GGGGCCCCAA	GACGAAGTGG	GCTCGGTGCT	360
GTACACCCGC	GGCGTGATCA	TCCAGATGCT	GGACAAGGTG	TCAATCACTA	AT	412

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TTGACACCTT	GTCCAGCATC	TGCATCTGAT	GAGAGCCTCA	GATGGCTACC	ACTAATGGCA	60
GAAGGCAAAG	GAGAACAGGC	ATTGTATGGC	AAGAAAGGAA	GAAAGAGAGA	GGGGAGAAAG	120
GTGCTAGGTT	CTTTTCAACA	ACCAATTCTT	GATGGAAGTG	AGAGTAAGAG	CTCAAGGCCA	180
GGTGTGGTGA	CTCCAACCAG	TAATCCCAAC	ATTTTAGGAG	GCTGAGGCAG	GCAGATGTCT	240
TGACCCCATG	AGTTTGTGAC	CAGCCTGAAC	AACATCATGA	GACTCCATCT	CTACAATAAT	300
TACAAAATT	AATCAGGCAT	TGTGGTATGC	CCTGTAGTCC	CAGATGCTGG	ACAAGGTGTC	360
A						361

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TWGACTGACT CATGTCCCCT ACACCCAACT ATCTTCTCCA GGTGGCCAGG CATGATAGAA	60
TCTGATCCTG ACTTAGGGGA ATATTTTCTT TTTACTTCCC ATCTTGATTC CCTGCCGGTG	120
AGTTTCCTGG TTCAGGGTAA GAAAGGAGCT CAGGCCAAAG TAATGAACAA ATCCATCCTC	180
ACAGACGTAC AGAATAAGAG AACWTGGACW TAGCCAGCAG AACMCAAKTG AAAMCAGAAC	240
MCTTAMCTAG GATRACAAMC MCRRARATAR KTGCCYCMCMC WTATAATAGA AACCAAACCTT	300
GTATCTAATT AAATATTTAT CCACYGTCAG GGCATTAGTG GTTTTGATAA ATACGCTTTG	360
GCTAGGATTC CTGAGGTTAG AATGGAARAA CAATTGCAMC GAGGGTAGGG GACATGAGTC	420
AKTCTAA	427

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AACGTCGCAT GCTCCCGGCC GCCATGGCCG CGGGATAGAC TGAATCATGT CCCCTAAGAT	60
AGAGGAGACA CCTGCTAGGT GTAAGGAGAA GATGGTTAGG TCTACGGAGG CTCCAGGGTG	120
GGAGTAGTTC CCTGCTAAGG GAGGGTAGAC TGTTCAACCT GTTCCTGCTC CGGCCTCCAC	180
TATAGCAGAT GCGAGCAGGA GTAGGAGAGA GGGAGGTAAG AGTCAGAAGC TTATGTTGTT	240
TATGCGGGGA AACGCCRTAT CGGGGGCAGC CRAGTTATTA GGGGACANTR TAGWYARTCW	300
AGNTAGCATC CAAAGCGNGG GAGTINTCCC ATATGGTTGG ACCTGCAGGC GGCCGCATTA	360
GTGATTAGCA TGTGAGCCCC AGACACGCAT AGCAACAAGG ACCTAAACTC AGATCCTGTG	420
CTGATTACTT AACATGAATT ATTGTATTTA TTTAACAACCT TTGAGTTATG AGGCATATTA	480
TTAGGTCCAT ATTACCTGGA	500

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TTCATCGCTC GGTGACTCAA GCCTGTAATC CCAGAACTTT GGGAGGCCGA GGGGAGCAGA	60
TCACCTGAGG TTGGGAGTTT GAGACCAGCC TGGCCAACAT GGTGACAACC CGTCTCTGCT	120
AAAAATACAA AAATTAGCCA AGCATGGTGG CATGCACTTG TAATCCCAGC TACTCGGGAG	180
GCTGAGGCAG GAGAATCACT TGAGGCCAGG AGGCAGAGGT TGCAGTGAGG CAGAGGTTGA	240
GATCATGCCA CTGCACTCCA GCCTGGGCAA CAGAGTAAGA CTCCATCTCA AAAAAAAAAA	300
AAAAAAGAA TGATCAGAGC CACAAATACA GAAAACCTTG AGTCACCGAG CGATGAAA	358

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

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TTCTGTCCAC ACCAATCTTA GAGCTCTGAA AGAATTTGTC TTAAATATC TTTTAATAGT      60
AACATGTATT TTATGGACCA AATTGACATT TTCGACTATT TTTTCCCAA AAAAGTCAGG      120
TGAATTTTCA CACACTGAGT TGGGAATTTC TTATCCAGA AGWCGGCACG AGCAATTTCA      180
TATTTATTTA AGATTGATTC CATACTCCGT TTTCAAGGAG AATCCCTGCA GTCTCCTTAA      240
AGGTAGAACA AATACTTTCT ATTTTTTTTT CACCATTGTG GGATTGGACT TTAAGAGGTG      300
ACTCTAAAAA AACAGAGAAC AAATATGTCT CAGTTGTATT AAGCACGGAC CCATATTATC      360
ATATTCACCT AAAAAAATGA TTTCTGTGTC ACCTTTTGGC AACTTCTCTT TTCAATGTAG      420
GGAAAAAACC AGTCACCCTG AAAACCCACA AAATAAATAA AACTTGTAGA TGTGGGCAGA      480
ARGTTTGGGG GTGGACATTG TATGTGTTTA AATTAAACCC TGTATCACTG AGAAGCTGTT      540
GTATGGGTCA GAGAAAATGA ATGCTTAGAA GCTGTTTACA TCTTCAAGAG CAGAAGCAAA      600
CCACATGTCT CAGCTATATT ATTATTTATT TTTTATGCAT AAAGTGAATC ATTTCTTCTG      660
TATTAATTTT CAAAGGGTTT TACCCTCTAT TTAAATGCTT TGAAAAACAG TGCATTGACA      720
ATGGGTTGAT ATTTTTCTTT AAAAGAAAAA TATAATTATG AAAGCCAAGA TAATCTGAAG      780
CCTGTTTTAT TTTAAACTT TTTATGTTCT GTGGTTGATG TTGTTTGTGT GTTTGTTTCT      840
ATTTTGTGGG TTTTTTACTT TGTTTTTGTG TTTGTTTTGT TTTGGTTTGD CATACTACAT      900
GCAGTTTCTT TAACCAATGT CTGTTTGGCT AATGTAATTA AAGTTGTTAA TTTATATGAG      960
TGCATTTCAA CTATGTCAAT GGTTTCTTAA TATTTATTGT GTAGAAGTAC TGGTAATTTT     1020
TTTATTTACA ATATGTTTAA AGAGATAACA GTTTGATATG TTTTCATGTG TTTATAGCAG     1080
AAGTTATTTA TTTCTATGGC ATTCCAGCGG ATATTTTGGT GTTTGCGAGG CATGCAGTCA     1140
ATATTTTGTA CAGTTAGTGG ACAGTATTCA GCAACGCCTG ATAGCTTCTT TGGCCTTATG     1200
TTAAATAAAA AGACCTGTTT GGGATGTAAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA     1260
AAAAA                                             1265

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(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

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TGTAAGTCGA GCAGTGTGAT GACGATATTC TTCTTATTAA TGTGGTAATT GAACAAATGA      60
TCTGTGATAC TGATCCTGAG CTAGGAGGCG CTGTTTCACTT AATGGGACTT CTTTCGTACTC     120
TAATTGATCC AGAGAACATG CTGGCTACAA CTAATAAAAC CGAAAAAAGT GAATTTCTAA      180
ATTTTTTCTA CAACCATTGT ATGCATGTTC TCACAGCACC ACTTTTGACC AATACTTCAG      240
AAGACAAATG TGAAAAGGAT AATATAGTTG GATCAAACAA AAACAACACA ATTTGTCCCG      300
ATAATTATCA AACAGCACAG CACTTGCCTT TAATTTTAGA GTTACTCACA TTTTGTGTGG      360
AACATCACAC TGCTCGACTT ACA                                             383

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(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGGGCACCTT CAATATCGCA AGTTAAAAAT AATGTTGAGT TTATTATACT TTTGACCTGT	60
TTAGCTCAAC AGGGTGAAGG CATGTAAAGA ATGTGGACTT CTGAGGAATT TTCTTTTAAA	120
AAGAACATAA TGAAGTAACA TTTTAATTAC TCAAGGACTA CTTTTGGTTG AAGTTTATAA	180
TCTAGATACC TCTACTTTTT GTTTTTGCTG TTCGACAGTT CACAAAGACC TTCAGCAATT	240
TACAGGGTAA AATCGTTGAA GTAGTGGAGG TGAAACTGAA ATTTAAAATT ATTCTGTAAA	300
TACTATAGGG AAAGAGGCTG AGCTTAGAAT CTTTTGGTTG TTCATGTGTT CTGTGCTCTT	360
ATCATCACAC TGCTCGACTT ACA	383

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

TCGGGTGATG CCTCCTCAGG CTTGTCGTTA GTGTACACAG AGCTGCTCAT GAAGCGACAG	60
CGGCTGCCCC TGGCACTTCA GAACCTCTTC CTCTACACTT TTGGTGCGCT TCTGAATCTA	120
GGTCTGCATG CTGGCGGCGG CTCTGGCCCA GGCCTCCTGG AAAGTTTCTC AGGATGGGCA	180
GCACTCGTGG TGCTGAGCCA GGCATAAAT GGACTGCTCA TGTCTGCTGT CATGGAGCAT	240
GGCAGCAGCA TCACACGCCT CTTGTGGTG TCCTGCTCGC TGGTGGTCAA CGCCGTGCTC	300
TCAGCAGTCC TGCTACGGCT GCAGCTCACA GCCGCCTTCT TCCTGGCCAC ATTGCTCATT	360
GGCCTGGCCA TGCGCCTGTA CTATGGCAGC CGCTAGTCCC TGACAACTTC CACCCTGATT	420
CCGGACCCTG TAGATTGGGC GCCACCACCA GATCCCCCTC CCAGGCCTTC CTCCCTCTCC	480
CATCAGCGGC CCTGTAAACA GTGCCTTGTT AGAAAAGCTG GAGAAGTGAG GGCAGCCAGG	540
TTATTCTCTG GAGGTTGGTG GATGAAGGGG TACCCCTAGG AGATGTGAAG TGTGGGTTTG	600
GTAAAGGAAA TGCTTACCAT CCCCCACCC CAACCAAGTT NTTCCAGACT AAAGAATTAA	660
GGTAACATCA ATACCTAGGC CTGAGGAGGC ATCACCCGA	699

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TCGGGTGATG CCTCCTCAGG CCAGATCAAA CTTGGGGTTG AAAACTGTGC AAAGAAATCA	60
ATGTCGGAGA AAGAATTTTG CAAAAGAAAA ATGCCTAATC AGTACTAATT TAATAGGTCA	120

CATTAGCAGT	GGAAGAAGAA	ATGTTGATAT	TTTATGTCAG	CTATTTTATA	ATCACCAGAG	180
TGCTTAGCTT	CATGTAAGCC	ATCTCGTATT	CATTAGAAAT	AAGAACAATT	TTATTCGTCG	240
GAAAGAACTT	TTCAATTTAT	AGCATCTTAA	TTGCTCAGGA	TTTTAAATTT	TGATAAAGAA	300
AGCTCCACTT	TTGGCAGGAG	TAGGGGGCAG	GGAGAGAGGA	GGCTCCATCC	ACAAGGACAG	360
AGACACCAGG	GCCAGTAGGG	TAGCTGGTGG	CTGGATCAGT	CACAACGGAC	TGACTTATGC	420
CATGAGAAGA	AACAACCTCC	AAATCTCAGT	TGCTTAATAC	AACACAAGCT	CATTTCTTGC	480
TCACGTTACA	TGTCCTATGT	AGATCAACAG	CAGGTGACTC	AGGGACCCAG	GCTCCATCTC	540
CATATGAGCT	TCCATAGTCA	CCAGGACACG	GGCTCTGAAA	GTGTCCTCCA	TGCAGGGACA	600
CATGCCTCTT	CCTTTCATTG	GGCAGAGCAA	GTCACCTATG	GCCAGAAGTC	ACACTGCAGG	660
GCAGTGCCAT	CCTGCTGTAT	GCCTGAGGAG	GCATCACCCG	A		701

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TCGGGTGATG	CCTCCTCANG	CCCCTAAATC	AGAGTCCAGG	GTCAGAGCCA	CAGGAGACAG	60
GGAAAGACAT	AGATTTTAAC	CGGCCCCCTT	CAGGAGATTG	TGAGGCTCAG	TTCACTTTGT	120
TGCAGTTTGA	ACAGAGGCAG	CAAGGCTAGT	GGTTAGGGGC	ACGGTCTCTA	AAGCTGCACT	180
GCCTGGATCT	GCCTCCCAGC	TCTGCCAGGA	ACCAGCTGCG	TGGCCTTGAG	CTGCTGACAC	240
GCAGAAAGCC	CCCTGTGGAC	CCAGTCTCCT	CGTCTGTAAG	ATGAGGACAG	GACTCTAGGA	300
ACCCTTTCCC	TTGGTTTGGC	CTCACTTTCA	CAGGCTCCCA	TCTTGAACTC	TATCTACTCT	360
TTTCTGAAA	CCTTGTAATA	GAAAAAAGTG	CTAGCCTGGG	CAACATGGCA	AAACCCTGTC	420
TCTACAAAAA	ATACAAAAAT	TAGTTGGGTG	TGGTGGCATG	TGCCTGTAGT	CCCAGCCACT	480
TGGGAGGTGC	TGAGGTGGGA	GGATCACTTG	AGCCCGGGAG	GTGGAGGTG	CAGTGAGCCA	540
AGATCATGCC	ACTGCACTCC	AGCCTGAGTA	ATAGAGTAAG	ACTCTGTCTC	AAAAACAACA	600
ACAACAACAG	TGAGTGTGCC	TCTGTTTCCG	GGTTGGATGG	GGCACCACAT	TTATGCATCT	660
CTCAGATTTG	GACGCTGCAG	CCTGAGGAGG	CATCACCCGA			700

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TATAGGGCGA	ATTGGGCCCC	AGTTGCATGN	TCCCGGCCGC	CATGGCCGCG	GGATTCGGGT	60
GATGCCTCCT	CAGGCTTGTC	TGCCACAAGC	TACTTCTCTG	AGCTCAGAAA	GTGCCCCCTG	120
ATGAGGGAAA	ATGTCCTACT	GCACTGCGAA	TTTCTCAGTT	CCATTTTACC	TCCCAGTCCT	180
CCTTCTAAAC	CAGTTAATAA	ATTCAATTCCA	CAAGTATTTA	CTGATTACCT	GCTTGTGCCA	240
GGGACTATTG	TCAGGCTGAA	GAAGGTGGGA	GGGGAGGGCG	GAACCTGAGG	AGCCACCTGA	300
GCCAGCTTTA	TATTTCAACC	ATGGCTGGCC	CATCTGAGAG	CATCTCCCCA	CTCTCGCCAA	360
CCTATCGGGG	CATAGCCAG	GGATGCCCCC	AGGCGGCCCA	GGTTAGATGC	GTCCCTTTGG	420
CTTGTCAGTG	ATGACATACA	CCTTAGCTGC	TTAGCTGGTG	CTGGCCTGAG	GAGGCATCAC	480
CCGA						484

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TCGGGTGATG CCTCCTCAGG GCTCAAGGGA TGAGAAGTGA CTTCTTTCTG GAGGGACCGT	60
TCATGCCACC CAGGATGAAA ATGGATAGGG ACCCACTTGG AGGACTTGCT GATATGTTTG	120
GACAAATGCC AGGTAGCGGA ATTGGTACTG GTCCAGGAGT TATCCAGGAT AGATTTTCAC	180
CCACCATGGG ACGTCATCGT TCAAATCAAC TCTTCAATGG CCATGGGGGA CACATCATGC	240
CTCCCACACA ATCGCAGTTT GGAGAGATGG GAGGCAAGTT TATGAAAAGC CAGGGGCTAA	300
GCCAGCTCTA CCATAACCAG AGTCAGGGAC TCTTATCCCA GCTGCAAGGA CAGTCGAAGG	360
ATATGCCACC TCGGTTTTCT AAGAAAGGAC AGCTTAATGC AGATGAGATT AGCCTGAGGA	420
GGCATCACCC GA	432

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 788 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

TAGCATGTTG AGCCCAGACA CAGTAGCATT TGTGCCAATT TCTGGTTGGA ATGGTGACAA	60
CATGCTGGAG CCAAGTGCTA ACATGCCTTG GTTCAAGGGA TGGAAAGTCA CCCGTAAGGA	120
TGGCAATGCC AGTGGAAACCA CGCTGCTTGA GGCTCTGGAC TGCATCCTAC CACCAACTCG	180
CCCAACTGAC AAGCCCTTGC GCCTGCCTCT CCAGGATGTC TACAAAATTG GTGGTATTGG	240
TACTGTTTCT GTTGGCCGAG TGGAGACTGG TGTTCTCAA CCCGGTATGG TGGTCACCTT	300
TGCTCCAGTC AACGTTACAA CGGAAGTAAA ATCTGTGCGAA ATGCACCATG AAGCTTTGAG	360
TGAAGCTCTT CCTGGGGACA ATGTGGGCTT CAATGTCAAG AATGTGTCTG TCAAGGATGT	420
TCGTGCTGGC AACGTTGCTG GTGACAGCAA AAATGACCCA CCAATGGAAG CAGCTGGCTT	480
CACTGCTCAG GTGATTATCC TGAACCATCC AGGCCAAATA AGTGCCGGCT ATGCCCCCTGT	540
ATTGGATTGC CACACGGCTC ACATTGCATG CAAGTTTGCT GAGCTGAAGG AAAAGATTGA	600
TCGCCGTTCT GGTAAAAAGC TGGAAGATGG CCCTAAATTC TTGAAGTCTG GTGATGCTGC	660
CATTGTTGAT ATGGTTCTCT GCAAGCCCAT GTGTGTTGAG AGCTTCTCAG ACTATCCACC	720
TTTGGGTCGC TTTGCTGTTT GTGATATGAG ACAGACAGTT GCGGTGGGTG TCTGGGCTCA	780
ACATGCTA	788

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TAGCATGTTG	AGCCCAGACA	CCTGTGTTTC	TGGGAGCTCT	GGCAGTGGCG	GATTCATAGG	60
CACTTGGGCT	GCACTTTGAA	TGACACACTT	GGCTTTATTA	GATTCACTAG	TTTTTAAAAA	120
ATTGTTGTTT	GTTTCTTTTC	ATTAAAGGTT	TAATCAGACA	GATCAGACAG	CATAATTTTG	180
TATTTAATGA	CAGAAACGTT	GGTACATTTT	TTCATGAATG	AGCTTGCATT	CTGAAGCAAG	240
AGCCTACAAA	AGGCACTTGT	TATAAATGAA	AGTTCTGGCT	CTAGAGGCCA	GTACTCTGGA	300
GTTTCAGAGC	AGCCAGTGAT	TGTTCCAGTC	AGTGATGCCT	AGTTATATAG	AGGAGGAGTA	360
CACTGTGCAC	TCTTCTAGGT	GTAAGGGTAT	GCAACTTTGG	ATCTTAAAAT	TCTGTACACA	420
TACACACTTT	ATATATATGT	ATGTATGTAT	GAAAACATGA	AATTAGTTTG	TCAAATATGT	480
GTGTGTTTAG	TATTTTAGCT	TAGTGCAACT	ATTTCCACAT	TATTTATTAA	ATTGATCTAA	540
GACACTTTCT	TGTTGACACC	TTGAATATTA	ATGTTCAAGG	GTGCAATGTG	TATTCCTTTA	600
GATTGTAAAA	GCTTAATTAC	TATGATTTGT	AGTAAATTAA	CTTTTAAAAT	GTATTTGAGC	660
CCTTCTGTAG	TGTCGTAGGG	CTCTTACAGG	GTGGGAAAGA	TTTAAATTTT	CCAGTTGCTA	720
ATTGAACAGT	ATGGCCTCAT	TATATATTTT	GATTTATAGG	AGTTTGTGTC	TGGGCTCAAC	780
ATGCTA						786

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TAGCATGTTG	AGCCCAGACA	CTGGTTACAA	GACCAGACCT	GCTTCCTCCA	TATGTAAACA	60
GCTTTTAAAA	AGCCAGTGAA	CCTTTTTAAT	ACTTTGGCAA	CCTTCTTTCA	CAGGCAAAGA	120
ACACCCCCAT	CCGCCCCCTG	TTTGGAGTGC	AGAGTTTGGC	TTTGGTTCTT	TGCCTTGCCT	180
GGAGTATACT	TCTAATTCCT	GTGTGCCTGC	ACAAGCTGAA	TACCGAGCTA	CCCACCGCCA	240
CCCAGGCCAG	GTTTCCACTC	ATTTATTACT	TTATGTTTCT	GTTCCATTGC	TGGTCCACAG	300
AAATAAGTTT	TCCTTTGGAG	GAATGTGATT	ATACCCCTTT	AATTTCCCTC	TTTTGCTTTT	360
TTTAAATATC	ATTGGTATGT	GTTTGGCCCA	GAGGAAACTG	AAATTCACCA	TCATCTTGAC	420
TGGCAATCCC	ATTACCATGC	TTTTTTTAAA	AAACGTAATT	TTTCTTGCCT	TACATTGGCA	480
GAGTAGCCCT	TCCTGGCTAC	TGGCTTAATG	TAGTCACTCA	GTTTCTAGGT	GGCATTAGGC	540
ATGAGACCTG	AAGCACAGAC	TGTCTTACCA	CAAAAGGTGA	CAAGATCTCA	AACCTTAGCC	600
AAAGGGCTAT	GTCAGGTTTC	AATGCTATCT	GCTTCTGTTC	CTGCTCACTG	TTCTGGATTT	660
TGTCCTTCTT	CATCCCTAGC	ACCAGAATTT	CCCAGTCTCC	CTCCCTACCT	TCCCTTGTTT	720
TAATTCTAAT	CTATCAGCAA	AATAACTTTT	CAAATGTTTT	AACCGGTATC	TCCATGTGTC	780
TGGGCTCAAC	ATGCTA					796

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGATGTGCTG	CAAGGCGATT	AAGTTGGGTA	ACGCCAGGGT	TTTCCCAGTC	ACGACGTTGT	60
AAAACGACGG	CCAGTGAATT	GTAATACGAC	TCACTATAGG	GCGAATTGGG	CCCGACGTCG	120
CATGCTCCCG	GCCGCCATGG	CCGCGGGATA	GCATGTTGAG	CCCAGACACC	TGCAGGTCAT	180
TTGGAGAGAT	TTTTCACGTT	ACCAGCTTGA	TGGTCTTTTT	CAGGAGGAGA	GACACTGAGC	240
ACTCCCAAGG	TGAGGTTGAA	GATTTCTCT	AGATAGCCCG	ATAAGAAGAC	TAGGAGGGAT	300
GCCTAGAAAA	TGATTAGCAT	GCAAATTTCT	ACCTGCCATT	TCAGAACTGT	GTGTCAGCCC	360
ACATTCAGCT	GCTTCTTG TG	AACTGAAAAG	AGAGAGGTAT	TGAGACTTTT	CTGATGGCCG	420
CTCTAACATT	GTAACACAGT	AATCTGTGTG	TGTGTGGGTG	TGTGTGTGTG	TCTGGGCTCA	480
ACATGCTA						488

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TAGCATGTTG	AGCCCAGACA	CGGCGACGGT	ACCTGATGAG	TGGGGTGATG	GCACCTGTGA	60
AAAGGAGGAA	CGTCATCCCC	CATGATATTG	GGGACCCAGA	TGATGAACCA	TGGCTCCGCG	120
TCAATGCATA	TTTAATCCAT	GATACTGCTG	ATTGGAAGGA	CCTGAACCTG	AAGTTTGTGC	180
TGCAGGTTTA	TCGGGACTAT	TACCTCACGG	GTGATCAAAA	CTTCCTGAAG	GACATGTGGC	240
CTGTGTGTCT	AGTAAGGGAT	GCACATGCAG	TGGCCAGTGT	GCCAGGGGTA	TGGTTCGTGT	300
CTGGGCTCAA	CATGCTA					317

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TAGCATGTTG	AGCCCAGACA	CTGGCTGTTA	GCCAAATCCT	CTCTCAGCTG	CTCCCTGTGG	60
TTTGGTGACT	CAGGATTACA	GAGGCATCCT	GTTTCAGGGA	ACAAAAAGAT	TTTAGCTGCC	120
AGCAGAGAGC	ACCACATACA	TTAGAATGGT	AAGGACTGCC	ACCTCCTTCA	AGAACAGGAG	180
TGAGGGTGGT	GGTGAATGGG	AATGGAAGCC	TGCATTCCCT	GATGCATTTG	TGCTCTCTCA	240
AATCCTGTCT	TAGTCTTAGG	AAAGGAAGTA	AAGTTTCAAG	GACGGTTCCG	AACTGCTTTT	300
TGTGTCTGGG	CTCAACATGC	TATCCCGCGG	CCATGGCGGC	CGGGAGCATG	CGACGTCGGG	360
CCCAATTCGC	CCTATAGTGA	GTCGTATTAC	AATTCAC TGG	CCGTCGTTTT	ACAACGTCGT	420
GACTGGGAAA	ACCCTGGCGT	TACCCAAC TT	AATCGCCTTG	CAGCACATCC	CCCTTTCCCA	480
GCTGGCGTAA	TANCGAAAAG	GCCCCGA				507

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATTTCGCT	GCAACACTGT	GGAGGTAGCC	CTGGAGCAAG	GCAGGCATGG	ATGCTTCTGC	60
AATCCCCAAA	TGGAGCCTGG	TATTTCAGCC	AGGAATCTGA	GCAGAGCCCC	CTCTAATTGT	120
AGCAATGATA	AGTTATTCTC	TTTGTTCTTC	AACCTTCCAA	TAGCCTTGAG	CTTCCAGGGG	180
AGTGTGTTA	ATCATTACAG	CCTGGTCTCC	ACAGTGTTC	AGCGTAA		227

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TTACGCTGCA	ACACTGTGGA	GCAGATTAAC	ATCAGACTTT	TCTATCAACA	TGACTGGGGT	60
TACTAAAAAG	ACAACAAATC	AATGGCTTCA	AAAGTCTAAG	GAATAATTTT	GATACTTCAA	120
CTTTATAAAA	CCTGACAAAA	CTATCAATCA	AGCATAAAGA	CAGATGAAGA	ACATTTCCAG	180
ATTTTGGCCA	ATCAGATATT	TTACCTCCAC	AGTGTTCAG	CGTAA		225

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGCCCGACGT	CGCATGCTCC	CGGCCGCCAT	GGCCGCGGGA	TTCGTTAGGG	TCTCTATCCA	60
CTGGGACCCA	TAGGCTAGTC	AGAGTATTTA	GAGTTGAGTT	CCTTTCTGCT	TCCCAGAATT	120
TGAAAGAAAA	GGAGTGAGGT	GATAGAGCTG	AGAGATCAGA	TTGCGCTCTG	AAGCCTGTTC	180
AAGATGTATG	TGCTCAGACC	CCACCACTGG	GGCCTGTGGG	TGAGGTCCTG	GGCATCTATT	240
TGAATGAATT	GCTGAAGGGG	AGCACTATGC	CAAGGAAGGG	GAACCCATCC	TGGCACTGGC	300
ACAGGGGTCA	CCTTATCCAG	TGCTCAGTGC	TTCTTTGCTG	CTACCTGGTT	TTCTCTCATA	360
TGTGAGGGGC	AGGTAAGAAG	AAGTGCCCRG	TGTTGTGCGA	GTTTTAGAAC	ATCTACCAGT	420
AAGTGGGGAA	GTTTCACAAA	GCAGCAGCTT	TGTTTTGTGT	ATTTTCACCT	TCAGTTAGAA	480
GAGGAAGGCT	GTGAGATGAA	TGTTAGTTGA	GTGGAAAAGA	CGGTAAGCT	TAGTGGATAG	540
AGACCCTAAC	GAATCACTAG	TGCGGCCGCC	TTGCAGGTCG	ACCATATGGG	AGAGCTC	597

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GGCCCGAAGT TGCATGTTCC CGGCCGCCAT GGCCGCGGGA TTCGTTAGGG TCTCTATCCA	60
CTACCTAAAA AATCCCAAAC ATATAACTGA ACTCCTCACA CCCAATTGGA CCAATCCATC	120
ACCCAGAGG CCTACAGATC CTCCTTTGAT ACATAAGAAA ATTTCCCAA ACTACCTAAC	180
TATATCATTT TGCAAGATTT GTTTTACCAA ATTTTGATGG CCTTTCTGAG CTTGTCAGTG	240
TGAACCACTA TTACGAACGA TCGGATATTA ACTGCCCTC ACCGTCCAGG TGTAGCTGGC	300
AACATCAAGT GCAGTAAATA TTCATTAAGT TTTCACCTAC TAAGGTGCTT AAACACCCTA	360
GGGTGCCATG TCGGTAGCAG ATCTTTTGAT TTGTTTTTAT TTCCCATAG GGTCTGTTC	420
AAGGTCAATC ATACATGTAG TGTGAGCAG TAGTCACTAT CGCATGACTT GGAGGGTGAT	480
AATAGAGGCC TCCTTTGCTG TTAAAGAACT CTTGTCCCAG CCTGTCAAAG TGGATAGAGA	540
CCCTAACGAA TCACTAGTGC GGCCGCCTGC AGGTCGACCA TATGGGAGAG CTCCCAA	597

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TCGTTAGGGT CTCTATCCAC TTGCAGGTAA AATCCAATCC TGTGTATATC TTATAGTCTT	60
CCATATGTAG TGGTTCAAGA GACTGCAGTT CCAGAAAGAC TAGCCGAGCC CATCCATGTC	120
TTCCAATTAA CCCTGCTTTG GGTTACACAT CTTAACTTTT CTGTTCAAGT TTCTCTGTGT	180
AGTTTATAGC ATGAGTATTG GGAWAATGCC CTGAAACCTG ACATGAGATC TGGGAAACAC	240
AAACTTACTC AATAAGAATT TCTCCCATAT TTTTATGATG GAAAAATTTC ACATGCACAG	300
AGGAGTGGAT AGAGACCCTA ACGA	324

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GCGCGGGGAT TCGGGGTGAT ACCTCCTCAT GCCAAAATAC AACGTNTAAT TTCACAACCTT	60
GCCTTCCAAT TTACGCATTT TCAATTTGCT CTCCCCATTT GTTGAGTCAC AACAAACACC	120
ATTGCCCAGA AACATGTATT ACCTAACATG CACATACTCT TAAAACTACT CATCCCTT	178

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TGACACCTTG	TCCAGCATCT	GACACAGTCT	TGGCTCTTGG	AAAATATTGG	ATAAATGAAA	60
ATGAATTTCT	TTAGCAAGTG	GTATAAGCTG	AGAATATACG	TATCACATAT	CCTCATTCTA	120
AGACACATTC	AGTGTCCCTG	AAATTAGAAT	AGGACTTACA	ATAAGTGTGT	TCACTTTCTC	180
AATAGCTGTT	ATTCAATTGA	TGGTAGGCCT	TAAAAGTCAA	AGAAATGAGA	GGGCATGTGA	240
AAAAAAGCTC	AACATCACTG	ATCATTAGAA	AACTTCCATT	CAAAACCCCA	ATGAGATACC	300
ATCTCATACC	AGTCAGAATG	GCTATTATTA	AAAAGTCAAA	AAATAACAGA	TGCTGGACAA	360
GGTGTCA						367

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GACACCTTGT	CCAGCATCTG	ACAACGCTAA	CAGCCTGAGG	AGATCTTTAT	TTATTTATTT	60
AGTTTTTACT	CTGGCTAGGC	AGATGGTGGC	TAAACATTC	ATTTACCCAT	TTATTCATTT	120
AATTGTTCTT	GCAAGGCCTA	TGGATAGAGT	ATTGTCCAGC	ACTGCTCTGG	AAGCTAGGAG	180
CATGGGGATG	AACAAGATAG	GCTACATCCT	GTTCCACAG	AACTTCCACT	TTAGTCTGGG	240
AAACAGATGA	TATATACAAA	TATATAAATG	AATTCAGGTA	GTTTAAAGTA	CGAAAAGAAT	300
AAGAAAGCAG	AGTCATGATT	TANAATGCTG	GAAACAGGGG	CTATTGCTTG	AGATATTGAA	360
GGTGCCCAA						369

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGACACCTTG	TCCAGCATCT	GCACAGGGAA	AAGAACTAT	TATCAGAGTG	AACAGGCAAC	60
CTACAGAATG	GGAGAAAATT	TTTGCAATCT	ATCCATCTGA	CAAAGGGCTA	ATATCCAGAA	120
TCTACAAAGA	ACTTATACAA	ATTTACAAGA	AACAAACAA	CAAACAACCTC	CTCAAAAAGT	180
GGGTGAAGGA	TGTGAACAGA	CACTTCTCAA	AAGAAGACAT	TTATGGGGCC	AACAAACATA	240
TGAAAAAAG	CTCATCATCA	CTGGTCACTA	GATAAATGCA	AATCAAAACC	ACAATGAGAT	300
ACCATCTCAT	TCCAGTTAGA	ATGGCAATCA	TTAAAAAGTC	AGGAAACAAC	AGATGCTGGA	360
CAAGGTGTC						369

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGACGCTTGG CCACTTGACA CTTTCATCTTT GCACAGAAAA ACTTCTTTAC AGATTTAATT	60
CAAGACTGGT CTAGTGACAG TCCTCCAGAC ATTTTTCAT TTGTTCCATA TACGTGGAAT	120
TTTAAAATCA TGTTTCATCA GTTTGAAATG ATTTGGGCTG CTAATCAACA CAATTGGATC	180
GACTGTTCTA CTAAACAACA GGAAAATGTG TATCTGGCAG CCTGTGGAGA AACACTAAAC	240
ATTGATTTT CTTTGCCTTT TACGGACTTT GTTCCAGCTA CATGTAATAC CAAGTTCTCT	300
TTAAGAGGAG AAGATGTTGA TCTTCATTTG TTTCTACCAG ACTGCCACCC TAGTAAATAT	360
TCTTTATTTA TGCTGGTAAA AAATTGCCAT CCAATAAGA TGATTCATGA TACTGGTATT	420
CCTGCTGAGT GTCAAGTGGC CAAGCGTCA	449

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGACGCTTGG CCACTTGACA CCAGGGATGT AKCAGTTGAA TATAATCCTG CAATTGTACA	60
TATTGGCAAT TTCCCATCAA ACATTCTAGA AAGAGACAAC CAGGATTGCT AGGCCATAAA	120
AGCTGCAATA AATAACTGGT AATTGCAGTA ATCATTTTCTG GCCAATTCAA TCCAGTTTGG	180
CTCAGAGGTG CCTTTGGCTG AGAGAAGAGG TGAGATATAA TGTGTTTCT TGCAACTTCT	240
TGGAAGAATA ACTCCACAAT AGTCTGAGGA CTAGATACAA ACCTATTTGC CATTAAAGCA	300
CCAGAGTCTG TTAATTCCAG TACTGATAAG TGTTGGAGAT TAGACTCCAG TGTGTCAAGT	360
GGCCAAGCGT CA	372

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGACGCTTGG CCACTTGACA CTTATGTAGA ATCCATCGTG GGCTGATGCA AGCCCTTTAT	60
TTAGGCTTAG TGTTGTGGGC ACCTTCAATA TCACACTAGA GACAAACGCC ACAAGATCTG	120
CAGAAACATT CAGTTCTGAN CACTCGAATG GCAGGATAAC TTTTGTGTT GTAATCCTTC	180
ACATATACAA AAACAACTC TGCANTCTCA CGTTACAAAA AAACGTACTG CTGTAAAATA	240
TTAAGAAGGG GTAAAGGATA CCATCTATAA CAAAGTAACT TACAAGTAGT GTCAAGTGGC	300
CAAGCGTCA	309

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TGACGCTTGG CCACTTGACA CCCAATCTCG CACTTCATCC TCCCAGCACC TGATGAAGTA	60
GGACTGCAAC TATCCCCACT TCCCAGATGA GGGGACCAAN GTACACATTA GGACCCGGAT	120
GGGAGCACAG ATTTGTCCGA TCCCAGACTC CAAGCACTCA GCGTCACTCC AGGACAGCGG	180
CTTTCAGATA AGGTCACAAA CATGAATGGC TCCGACAACC GGAGTCAGTC CGTGCTGAGT	240
TAAGGCAATG GTGACACGGA TGCACGTGTN ACCTGTAATG GTTCATCGTA AGTGTC AAGT	300
GGCCAAGCGT CA	312

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TGTATCGACG TAGTGGTCTC CTCAGCCATG CAGAACTGTG ACTCAATTAA ACCTCTTTCC	60
TTTATGAATT ACCCAATCTC GGGTAGTGTC TTTATAGTAG TGTGAGAATG GACTAATACA	120
AGTACATTTT ACTTAGTAAT AATAATAAAC AAATATATTA CATTTTGTG TATTTACTAC	180
ACCATATTTT TTATTGTTAT TGTAAGTGTAC ACCTTCTACT TATTAAAAGA AATAGGCCCG	240
AGGCGGGCAG ATCACCAGGT CAGGAGATGG AGACCACTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTGGGCACCT TCAATATCAT GACAGGTGAT GTGATAACCA AGAAGGCTAC TAAGTGATTA	60
ATGGGTGGGT AATGTATACA GAGTAGGTAC ACTGGACAGA GGGGTAATTC ATAGCCAAGG	120
CAGGAGAAGC AGAATGGCAA AACATTTCAT CACACTACTC AGGATAGCAT GCAGTTTAA	180
ACCTATAAGT AGTTTATTTT TGAATTTTC CACTTAATAT TTTCAGACTG CAGGTAAC	240
AACTGTGGAA CACAAGAACA TAGATAAGGG GAGACCACTA CGTCGATAC	289

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GTATCGACGT AGTGGTCTCC CAAGCAGTGG GAAGAAAACG TGAACCAATT AAAATGTATC	60
AGATACCCCA AAGAAAGGCG CTGAGTAAA GATTCCAAGT GGGTCACAAT CTCAGATCTT	120
AAAATTCAGG CTGTCAAAGA GATTGCTAT GAGGTTGCTC TCAATGACTT CAGGCACAGT	180
CGGCAGGAGA TTGAAGCCCT GGCCATTGTC AAGATGAAGG AGCTTTGTGC CATGTATGGC	240
AAGAAAGACC CCAATGAGCG GGA CTCTGG AGACCACTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTTTTTGGG AAAAACNCAA NTGGGGGAAA GGGGNTTNN TNGCAAGGGG ATAAAGGGGG	60
AANCCCAGGG TTTCCCATC CAGGGAGGTG TAAAAAGNCG GCCAGGGGAT TGTAANAGGA	120
TTCAATAATA GGGGGAATGG GCCCNGAAGT TGCAAGGTTC CNGCCCGCCA TGNCCGCGGG	180
ATTTAGTGAC ATTACGACGS TGGTAATAAA GTGGGSCCAA WAAATATTTG TGATGTGATT	240
TTTSGACCAG TGAACCCATT GWACAGGACC TCATTTCTCY TGAGATGRTA GCCATAATCA	300
GATAAAAGRT TAGAAGTYTT TCTGCACGTT AACAGCATCA TTAAATGGAG TGGCATCACC	360
AATTTACCCC TTTGTTAGCC GATACCTTCC CCTTGAAGGC ATTCAATTAA GTGACCAATC	420
GTCATACGAG AGGGGATGGC ATGGGGATTG ATGATGATAT CAGGGGTGAT ACCTTCACAG	480
GTGAAAGGCA TATCCTCTTG TCTATACTGA ATACCACAAG TACCCTTTTG ACCATGTCGA	540
CTAGCAAATT TGTCTCCAAT CTGTGTWATC CCTAACAGAG CGTACCCTTA TTTTACAAAA	600
TTTATATCCT TCCTGATTGA GAGTTACCAT AACCTGATCC ACAATGCCCC TCTCGCTWGT	660
TCTGAGAAAA GTGCTACAGT CTCTCTTGGT ATAGCGTCTA TTGGTGCTCT CCAATTCATC	720
TTCATTTTTC AGGCAAGGTG AACTGTTTTG CCTATAATAA CMTCATCTCC TGATACMCGA	780
AACCCCKGGA RCTATCAAA CATCATCATC CAGCGTCTKT WATGYMCTA AATCCCTATT	840
GCGGCCGCCT GCAGGTCAAC ATATNGGAAA ACCCCCCACC CCTTNGGAGC NTACCTTGAA	900
TTTCCATAT GTCCCNATAA TTANCTNGNC TTANCTGGC CNTAACCTNT TCCGGTTTAA	960
ATTGTTTCCG CCCCNTTCC CCNCCTTNA ACCGGAAACC TTAATTTTNA ACCNNGGGTT	1020
CCTATCC	1027

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

AGTGACATTA CGACGCTGGC CATCTTGAAT CCTAGGGCAT GAAGTTGCCC CAAAGTTCAG	60
CACTTGGTTA AGCCTGATCC CTCTGGTTTA TCACAAAGAA TAGGATGGGA TAAAGAAAGT	120
GGACACTTAA ATAAGCTATA AATTATATGG TCCTTGTCTA GCAGGAGACA ACTGCACAGG	180

TATACTACCA GCGTCGTAAT GTCACTA

207

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TGGGCACCTT CAATATCTAT TAAAAGCACA AATACTGAAG AACACACCAA GACTATCAAT	60
GAGGTTACAT CTGGAGTCCT CGATATATCA GGAAAAAATG AAGTGAACAT TCACAGAGTT	120
TTACTTCTTT GGGAAGTCAA ATGCTAGAAA AGAAAAGGGT GCCCTCTTTC TCTGGCTTCC	180
TGGTCCTATC CAGCGTCGTA ATGTCACTA	209

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

NTACGCTGCA ACACTGTGGA GCCACTGGTT TTTATTCCCG GCAGGTTATC CAGCAAACAG	60
TCACTGAACA CACCGAAGAC CGTGGTATGG TAACCGTTCA CAGTAATCGT TCCAGTCGTC	120
TGCGGGACCC CGACGAGCGT CACTGGGTAC AGACCAGATT CAGCCGGAAG AGAAAGCGCC	180
GCAGGGAGAG ACTCGAAGTC CACTCCGCTG GTGAGCAGCC CCATGTTTTC AACTCGAAGT	240
TCAAACGGCA TTGGGTTATA TACCATCAGC TGAAC TTCAC ACACATCTCC TTGAACCCAC	300
TGGAAATCTA TTTTCTTGTT CCGCTCTTCT CCACAGTGTT GCAGCGTAA	349

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TGCTCCTCTT GCCTTACCAA CCCAAAGCCC ACTGTGAAAT ATGAAGTGAA TGACAAAATT	60
CAGTTTTCAA CGCAATATAG TATAGTTTAT CTGATTCTTT TGATCTCCAG GACACTTTAA	120
ACAACTGCTA CCACCACCAC CAACCTAGGG ATTTAGGATT CTCCACAGAC CAGAAATTAT	180
TTCTCCTTTG AGTTTCAGGC TCCTCTGGGA CTCCTGTTCA TCAATGGGTG GTAAATGGCT	240
A	241

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TAGCCATTTA CCACCCATCT GCAAACCSWG ACMWWCARGR CYWGWACKYA GGCGATTTGA	60
AGTACTGGTA ATGCTCTGAT CATGTTAGTT ACATAAGTGT GGTCAGTTTA CAAAAATTCA	120
CAGAACTAAA TACTCAATGC TATGTGTTCA TGTCTGTGTT TATGTGTGTG TAATGTTTCA	180
ATTAAGTTTT TTTAAAAAAA AGAGATGATT TCCAAATAAG AAAGCCGTGT TGTAAGGCA	240
AGAGGAGC	248

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TACGCTGCAA CACTGTGGAG CCATTCATAC AGGTCCCTAA TTAAGGAACA AGTGATTATG	60
CTACCTTTGC ACGGTTAGGG TACCGCGGCC GTTAAACATG TGTCAGTGGG CAGGCGGTGC	120
CTCTAATACT GGTGATGCTA GAGGTGATGT TTTTGGTAAA CAGGCGGGGT AAGATTTGCC	180
GAGTTCCTTT TACTTTTTTT AACCTTTCCT TATGAGCATG CCTGTGTTGG GTTGACAGTG	240
GGGGTAATAA TGACTTGTTG GTTGATTGTA GATATTGGGC TGTTAATTGT CAGTTCAGTG	300
TTTTAATCTG ACGCAGGCTT ATGCGGAGGA GAATGTTTC ATGTTACTTA TACTAACATT	360
AGTTCTTCTA TAGGGTGATA GATTGGTCCA ATTGGGTGTG AGGAGTTCAG TTATATGTTT	420
GGGATTTTTT AGGTAGTGGG TGTTGANCTT GAACGCTTTC TTAATTGGTG GCTGCTTTTA	480
RGCCTACTAT GGGTGGTAAA TGGCT	505

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TAGACTGACT CATGTCCCCT ACCAAAGCCC ATGTAAGGAG CTGAGTTCTT AAAGACTGAA	60
GACAGACTAT TCTCTGGAGA AAAATAAAAT GGAAATTGTA CTTTAAAAAA AAAAAAATC	120
GGCCGGGCAT GGTAGCACAC ACCTGTAATC CCAGCTACTA GGGGACATGA GTCAGTCTA	179

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AGACTGACTC ATGTCCCCTA CCCCACCTTC TGCTGTGCTG CCGTGTTCCT AACAGGTCAC	60
AGACTGGTAC TGGTCAGTGG CCTGGGGGTT GGGGACCTCT ATTATATGGG ATACAAATTT	120
AGGAGTTGGA ATTGACACGA TTTAGTGACT GATGGGATAT GGGTGGTAAA TGGCTA	176

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGACTGACTC ATGTCCCCTA TTAAACAGGG TCTCTAGTGC TGTGAAAAAA AAAAATGCTG	60
AACATTGCAT ATAACCTATA TTGTAAGAAA TACTGTACAA TGACTTTTATT GCATCTGGGT	120
AGCTGTAAGG CATGAAGGAT GCCAAGAAGT TTAAGGAATA TGGGTGGTAA ATGGCTAGGG	180
GACATGAGTC AGTCTA	196

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GACGCTTGGC CACTTGACAC CTTTATTTTT TTAAGGATTC TTAAGTCATT TANGTNACTT	60
TGTAAGTTTT TCCTGTGCCC CCATAAGAAT GATAGCTTTA AAAATTATGC TGGGGTAGCA	120
AAGAAGATAC TTCTAGCTTT AGAATGTGTA GGTATAGCCA GGATTCTTGT GAGGAGGGGT	180
GATTTAGAGC AAATTTCTTA TTCTCCTTGC CTCATCTGTA ACATGGGGAT AATAATAGAA	240
CTGGCTTGAC AAGGTTGGAA TTAGTATTAC ATGGTAAATA CATGTAAAT GTTTAGAATG	300
GTGCCAAGTA TCTAGGAAGT ACTTGGGCAT GGGTGGTAAA TGGCT	345

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GACGCTTGGC	CACTTGACAC	TAGAGTAGGG	TTTGGCCAAC	TTTTTCTATA	AAGGACCAGA	60
GAGTAAATAT	TTCAGGCTTT	GTGGGTGTG	CAGTCTCTCT	TGCAACTACT	CAGCTCTGCC	120
ATTGTAGCAT	AGAAATCAGC	CATAGACAGG	ACAGAAATGA	ATGGGTGGTA	AATGGCTA	178

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGGGCACCTT	CAATATCTAT	CCAGCGCATC	TAAATTCGCT	TTTTTCTTGA	TTAAAAATTT	60
CACCACTTGC	TGTTTTTGCT	CATGTATACC	AAGTAGCAGT	GGTGTGAGGC	CATGCTTGTT	120
TTTTGATTGC	ATATCAGCAC	CGTATAAGAG	CAGTGCTTTG	GCCATTAATT	TATCTTCATT	180
GTAGACAGCA	TAGTGTAGAG	TGGTATCTCC	ATACTCATCT	GGAATATTTG	GATCAGTGCC	240
ATGTTCCAGC	AACATTAACG	CACATTCATC	TTCTTGGCAT	TGTACGGCCT	TTGTCAGAGC	300
TGTCCTCTTT	TTGTTGTCAA	GGACATTAAG	TTGACATCGT	CTGTCCAGCA	CGAGTTTTAC	360
TACTTCTGAA	TTCCCATTTG	CAGAGGCCAG	ATGTAGAGCA	GTCCTCTTTT	GCTTGTCCCT	420
CTTGTTTACA	TCAGTGTCCC	TGAGCATAAC	GGAA			454

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCCGTTATGC	CACCCAGAAA	ACCTACTGGA	GTTACTTATT	AACATCAAGG	CTGGAACCTA	60
TTTGCCTCAG	TCCTATCTGA	TTCATGAGCA	CATGGTTATT	ACTGATCGCA	TTGAAAACAT	120
TGATCACCTG	GGTTTCTTTA	TTTATCGACT	GTGTCATGAC	AAGGAACTT	ACAACTGCA	180
ACGCAGAGAA	ACTATTAAAG	GTATTCAGAA	ACGTGAAGCC	AGCAATTGTT	TCGCAATTGC	240
GCATTTTGAA	AACAAATTTG	CCGTGGAAAC	TTTAATTTGT	TCTTGAACAG	TCAAGAAAAA	300
CATTATTGAG	GAAAATTAAT	ATCACAGCAT	AACGGAA			337

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TCGGGTGATG	CCTCCTCAGG	CATCTTCCAT	CCATCTCTTC	AAGATTAGCT	GTCCCAAATG	60
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TTTTTCCTTC	TCTTCTTTAC	TGATAAATTT	GGACTCCTTC	TTGACACTGA	TGACAGCTTT	120
AGTATCCTTC	TTGTACCTT	GCAGACTTTA	AACATAAAAA	TACTCATTGG	TTTTAAAAGG	180
AAAAAAGTAT	ACATTAGCAC	TATTAAGCTT	GGCCTTGAAA	CATTTTCTAT	CTTTTATTAA	240
ATGTCGGTTA	GCTGAACAGA	ATTCATTTTA	CAATGCAGAG	TGAGAAAAGA	AGGGAGCTAT	300
ATGCATTTGA	GAATGCAAGC	ATTGTCAAAT	AAACATTTTA	AATGCTTTCT	TAAAGTGAGC	360
ACATACAGAA	ATACATTAAG	ATATTAGAAA	GTGTTTTTGC	TTGTGTACTA	CTAATTAGGG	420
AAGCACCTTG	TATAGTTCCT	CTTCTAAAAT	TGAAGTAGAT	TTTAAAAACC	CATGTAATTT	480
AATTGAGCTC	TCAGTTCAGA	TTTTAGGAGA	ATTTTAACAG	GGATTTGGTT	TTGTCTAAAT	540
TTTGTCAATT	TNTTTAGTTA	ATCTGTATAA	TTTTATAAAT	GTCAAACGTG	ATTTAGTCCG	600
TTTTCATGCT	GCTATGAAAG	AAATACCCAN	GACAGGGTTA	TTTATAAANG	GAAAGANGTT	660
AATTTGACTC	CCAGTTCACA	GGCCTGAGGA	NGNATCNCCC	GAAATCCTTA	TTGCG	715

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GGTAANGNGC	ATACNTCGGT	GCTCCGGCCG	CCGGAGTCGG	GGGATTCGGG	TGATGCCTCC	60
TCAGGCCAC	TTGGGCCTGC	TTTTCCCAA	TGGCAGCTCC	TCTGGACATG	CCATTCCTTC	120
TCCCACCTGC	CTGATTCTTC	ATATGTTGGG	TGTCCCTGTT	TTTCTGGTGC	TATTTCTCTGA	180
CTGCTGTTCA	GCTGCCACTG	TCCTGCAAAG	CCTGCCTTTT	TAAATGCCTC	ACCATTCCCTT	240
CATTTGTTTC	TTAAATATGG	GAAGTGAAAG	TGCCACCTGA	GGCCGGGCAC	AGTGGCTCAC	300
GCCTGTAATC	CCAGCACTTT	GGGAGCCTGA	GGAGGCATCA	CCCGA		345

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GGTGATGCCT	CCTCAGGCGA	AGCTCAGGGA	GGACAGAAAC	CTCCCGTGGA	GCAGAAGGGC	60
AAAAGCTCGC	TTGATCTTGA	TTTTCAGTAC	GAATACAGAC	CGTGAAAGCG	GGGCCTCACG	120
ATCCTTCTGA	CCTTTTGGGT	TTTAAGCAGG	AGGTGTCAGA	AAAGTTACCA	CAGGGATAAC	180
TGGCTTGTGG	CGGCCAAGCG	TTCATAGCGA	CGTCGCTTTT	TGATCCTTCG	ATGTCGGCTC	240
TTCCTATCAT	TGTGAAGCAG	AATTCACCAA	GCGTTGGATT	GTTCACCCAC	TAATAGGGAA	300
CGTGAGCTGG	GTTTAGACCG	TCGTGAGACA	GGTTAGTTTT	ACCCTACTGA	TGATGTGTGK	360
TTGCCATGGT	AATCCTGCTC	AGTACGAGAG	GAACCGCAGG	TTCASACATT	TGGTGTATGT	420
GCTTGCCTT						429

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGACACCTAT	GTCCNGCATC	TGTTACAGT	TTCCACAAAT	AGCCAGCCTT	TGGCCACCTC	60
TCTGTCCTGA	GGTATACAAG	TATATCAGGA	GGTGTATACC	TTCTCTTCTC	TTCCCCACCA	120
AAGAGAACAT	GCAGGCTCTG	GAAGCTGTCT	TAGGAGCCTT	TGGGCTCAGA	ATTTTCAGAGT	180
CTTGGGTACC	TTGGATGTGG	TCTGGAAGGA	GAAACATTGG	CTCTGGATAA	GGAGTACAGC	240
CGGAGGAGGG	TCACAGAGCC	CTCAGCTCAA	GCCCCTGTGC	CTTAGTCTAA	AAGCAGCTTT	300
GGATGAGGAA	GCAGGTTAAG	TAACATACGT	AAGCGTACAC	AGGTAGAAAG	TGCTGGGAGT	360
CAGAATTGCA	CAGTGTGTAG	GAGTAGTACC	TCAATCAATG	AGGGCAAATC	AACTGAAAGA	420
AGAAGACCNA	TTAATGAATT	GCTTANGGGG	AAGGATCAAG	GCTATCATGG	AGATCTTTCT	480
AGGAAGATTA	TTGTTTANAA	TTATGAAAGG	ANTAGGGCAG	GGACAGGGCC	AGAAGTANAA	540
GANAACATTG	CCTATANCCC	TTGTCTTGCA	CCCAGATGCT	GGACAAGGTG	TCA	593

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TGACACCTTG	TCCAGCATCT	GACGTGAAGA	TGAGCAGCTC	AGAGGAGGTG	TCCTGGATTT	60
CCTGGTTCTG	TGGGCTCCGT	GGCAATGAAT	TCTTCTGTGA	AGTGGATGAA	GACTACATCC	120
AGGACAAATT	TAATCTTACT	GGACTCAATG	AGCAGGTCCC	TCACTATCGA	CAAGCTCTAG	180
ACATGATCTT	GGACCTGGAG	CCTGATGAAG	AACTGGAAGA	CAACCCCAAC	CAGAGTGACC	240
TGATTGAGCA	GGCAGCCGAG	ATGCTTTATG	GATTGATCCA	CGCCCGCTAC	ATCCTTACCA	300
ACCGTGGCAT	CGCCAGATG	CTGGACAAGG	TGTCA			335

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TACGTACTGG	TCTTGAAGGT	CTTAGGTAGA	GAAAAAATGT	GAATATTTAA	TCAAAGACTA	60
TGTATGAAAT	GGGACTGTAA	GTACAGAGGG	AAGGGTGGCC	CTTATCGCCA	GAAGTTGGTA	120
GATGCGTCCC	CGTCATGAAA	TGTTGTGTCA	CTGCCCGACA	TTTGCCGAAT	TACTGAAATT	180
CCGTAGAATT	AGTGCAAATT	CTAACGTTGT	TCATCTAAGA	TTATGGTTCC	ATGTTTCTAG	240
TACTTTTA						248

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGACGCTTGG	CCACTTGACA	CAAGTAGGGG	ATAAGGACAA	AGACCCATNA	GGTGGCCTGT	60
CAGCCTTTTG	TTACTGTTGC	TTCCCTGTCA	CCACGGCCCC	CTCTGTAGGG	GTGTGCTGTG	120
CTCTGTGGAC	ATTGGTGCAT	TTTCACACAT	ACCATCTCT	TTCTGCTTCA	CAGCAGTCCT	180
GAGGCGGGAG	CACACAGGAC	TACCTTGTC	GATGANGATA	ATGATGTCTG	GCCAACTCAC	240
CCCCCAACCT	TCTCACTAGT	TATANGAAGA	GCCANGCCTA	NAACCTTCTA	TCCTGNCCCC	300
TTGCCCTATG	ACCTCATCCC	TGTTCCATGC	CCTATTCTGA	TTTCTGGTGA	ACTTTGGAGC	360
AGCCTGGTTT	NTCCTCCTCA	CTCCAGCCTC	TCTCCATACC	ATGGTANGGG	GGTGCTGTTC	420
CACNCAAANG	GTCAGGTGTG	TCTGGGGAAT	CCTNANANCT	GCCNGGAGTT	TCCNANGCAT	480
TCTTAAAAAC	CTTCTTGCCT	AATCANATNG	TGTCCAGTGG	CCAACNTCN		530

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGACGCTTGG	CCACTTGACA	CTAAATAGCA	TCTTCTAAAG	GCCTGATTCA	GAGTTGTGGA	60
AAATTCTCCC	AGTGTGAGGG	ATTGTCAGGA	ACAGGGCTGC	TCCTGTGCTC	ACTTTACCTG	120
CTGTGTTTCT	GCTGGAAAAG	GAGGGAAGAG	GAATGGCTGA	TTTTTACCTA	ATGTCTCCCA	180
GTTTTCATA	TTCTTCTTGG	ATCCTCTTCT	CTGACAACCTG	TTCCCTTTTG	GTCTTCTTCT	240
TCTTGCTCAG	AGAGCAGGTC	TCTTTAAAC	TGAGAAGGGA	GAATGAGCAA	ATGATTAAAG	300
AAAACACACT	TCTGAGGCCC	AGAGATCAAA	TATTAGGTAA	ATACTAAACC	GCTTGCCTGC	360
TGTGGTCACT	TTTCTCCTCT	TTCACATGCT	CTATCCCTCT	ATCCCCCACC	TATTCATATG	420
GCTTTTATCT	GCCAAGTTAT	CCGGCCTCTC	ATCAACCTTC	TCCCCTAGCC	TACTGGGGGA	480
TATCCATCTG	GGTCTGTCTC	TGGTGTATTG	GTGTCAAGTG	GCCAAGCGTC	A	531

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ATTGACGCTT	GGCCACTTGA	CACCCGCCTG	CCTGCAATAC	TGGGGCAAGG	GCCTTCACTG	60
CTTTCCTGCC	ACCAGCTGCC	ACTGCACACA	GAGATCAGAA	ATGCTACCAA	CCAAGACTGT	120
TGGTCCTCAG	CCTCTCTGAG	GAGAAAGAGC	AGAAGCCTGG	AAGTCAGAAG	AGAAGCTAGA	180
TCGGCTACGG	CCTTGGCAGC	CAGCTTCCCC	ACCTGTGGCA	ATAAAGTCGT	GCATGGCTTA	240
ACAATGGGGG	CACCTCCTGA	GAAACACATT	GTTAGGCAAT	TCGGCGTGTG	TTCATCAGAG	300

CATATTTACA CAAACCTCGA TAGTGCAGCC TACTATCCAC TATTGCTCCT ACGCTGCAAA	360
CCTGAACAGC ATGGGACTGT ACTGAATACT GGAAGCAGCT GGTGATGGTA CTTATTTGTG	420
TATCTAAACA CAGAGAAGGT ACAGTAAGAA TATGGTATCA TAAACTTACA GGGACCGCCA	480
TCCTATATGC AGTCTGTTGT GACCAAAATG TGTCAAGTGG CCAAGCGTCA	530

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTATCGACG TAGTGGTCTC CGGGCTACTA GGCCGTTGTG TGCTGGTAGT ACCTGGTTCA	60
CTGAAAGGCG CATCTCCCTC CCCGCGTCGC CCTGAAGCAG GGGGAGGACT TCGCCCAGCC	120
AAGGCAGTTG TATGAGTTTT AGCTGCGGCA CTTGAGACC TCTGAGCCCA CCTCCTTCAG	180
GAGCCTTCCC CGATTAAGGA AGCCAGGGTA AGGATTCCTT CCTCCCCCAG ACACCACGAA	240
CAAACCACCA CCCCCCTAT TCTGGCAGCC CATATACATC AGAACGAAAC AAAAATAACA	300
AATAAACNAA AACCAGAAAA AAAAGAGAAG GGGAAATGTA TATGTCTGTC CATCCTGTTG	360
CTTTAGCCTG TCAGCTCCTA NAGGGCAGGG ACCGTGTCTT CCGAATGGTC TGTGCAGCGC	420
CGACTGCGGG AAGTATCGGA GGAGGAAGCA GAGTCAGCAG AAGTTGAACG GTGGGCCCCG	480
CGGCTCTTGG GGGCTGGTGT TGTACTTCGA GACCGCTTTC GCTTTTGTGTC TTAGATTTAC	540
GTTTGCTCTT TGGAGTGGGA NACCACTACN TCNATACA	578

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGTATCGACG TAGTGGTCTC CTCTTGCAAA GGACTGGCTG GTGAATGGTT TCCCTGAATT	60
ATGGACTTAC CCTAAACATA TCTTATCATC ATTACCAGTT GCAAAATATT AGAATGTGTT	120
GTCAGTGTTC CATTTGATTC CTAGAAGGTT AGTCTTAGAT ATGTTACTTT AACCTGTATG	180
CTGTAGTGCT TTGAATGCAT TTTTGTGTTG CATTTTGTGTT TGCCCAACCT GTCAATTATA	240
GCTGCTTAGG TCTGGACTGT CCTGGATAAA GCTGTTAATAA TATTCACCAG TCCAGCCATC	300
TTACAAGCTA ATTAAGTCAA CTAAATGCTT CCTTGTTTTG CCAGACTTGT TATGTCAATC	360
CTCAATTTCT GGGTTCATTT TGGGTGCCCT AAATCTTAGG GTGTGACTTT CTTAGCATCC	420
TGTAACATCC ATTCCCAAGC AAGCACAAC TACATAATA CTTTCCAGAA GTTCATTGCT	480
GAAGCCTTTC CTTACCCAG CGGAGCAACT TGATTTTCTA CAACTTCCCT CATCAGAGCC	540
ACAAGAGTAT GGGATATGGA GACCACTACG TCGATACA	578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGTATCGACG TANTGGTCTC CCAAGGTGCT GGGATTGCAG GCATGAGCCA CCACTCCCAG	60
GTGGATCTTT TTCTTTATAC TTACTTCATT AGGTTTCTGT TATTCAAGAA GTGTAGTGGT	120
AAAAGTCTTT TCAATCTACA TGGTTAAATA ATGATAGCCT GGGAAATAAA TAGAAATTTT	180
TTCTTTCATC TTTAGGTTGA ATAAAGAAAC AGAAAAATA GAACATACTG AAAATAATCT	240
AAGTTCCAAC CATAGAAGAA CTGCAGAAGA AATGAAGAAA GTGATGATGA TTTAGATTTT	300
GATATTGATT TAGAAGACAC AGGAGGAGAC CACTACGTCG ATACA	345

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TGTATCGACG TAGTGGTCTC CAAACTGAGG TATGTGTGCC ACTAGCACAC AAAGCCTTCC	60
AACAGGGACG CAGGCACAGG CAGTTTAAAG GGAATCTGTT TCTAAATTAA TTTCCACCTT	120
CTCTAAGTAT TCTTTCCTAA AACTGATCAA GGTGTGAAGC CTGTGCTCTT TCCCAACTCC	180
CCTTTGACAA CAGCCTTCAA CTAACACAAG AAAAGGCATG TCTGACACTC TTCCTGAGTC	240
TGACTCTGAT ACGTTGTTCT GATGTCTAAA GAGCTCCAGA ACACCAAAGG GACAATTACG	300
AATGCTGGTG TATAACAGAC TCCAATGGAG ACCACTACGT CGATACA	347

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

AGGNGNGGGA NTGTATCGAC GTAGTGGTCT CCCAACAGTC TGTCATTAGC TCTGCAGGTG	60
TCAGTGTTTT GGACAATGAG GCACCATGT CACTTATTGA CTCCTCAGCT CTAAATGCTG	120
AAATTAAATC TTGTCATGAC AAGTCTGGAA TTCCTGATGA GGTTTTACAA AGTATTTTGG	180
ATCAATACTC CAACAAATCA GAAAGCCAGA AAGAGGATCC TTTCAATATT GCAGAACCAC	240
GAGTGGATTT ACACACCTCA GGAGACCACT ACGTCGATAC A	281

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGGAAACACT TCCTCCCAGC CTTGTAAGGG TTGGAGCCCT CTCCAGTATA TGCTGCAGAA	60
TTTTTCTCTC GGTCTCTCAG AGGATTATGG AGTCCGCCTT AAAAAAGGCA AGCTCTGGAC	120
ACTCTGCAAA GTAGAATGGC CAAAGTTTGG AGTTGAGTGG CCCCTTGAAG GGTCAGTAA	180

CCTCACAATT	GTTCAAGCTG	TGTGGCGGGT	TGTTACTGAA	ACTCCCGGCC	TCCCTGATCA	240
GTTTCCCTAC	ATTGATCAAT	GGCTGAGTTT	GGTCAGGAGC	ACCCCTTCCG	TGGCTCCACT	300
CATGCACCAT	TCATAATTTT	ACCTCCAAGG	TCCTCCTGAG	CCAGACCGTG	TTTTCGCCTC	360
GACCCTCAGC	CGGTTCCGGCT	CGCCCTGTAC	TGCTCTCTCT	TGAAGAAGAG	GAGAGTCTCC	420
CTCACCCAGT	CCCACCGCCT	TAAAACCAGC	CTACTCCCTT	AGGGTCATCC	CATGTCTCCT	480
CGGCTATGTC	CCCTGTAGGC	TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	TGGTGGGAGG	540
AAGTAGCCCC	TCTACTACCA	CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	600
CCCCCTTCCT	GGTTTATGTC	CCTTCTTTCT	ACTTCTGACT	TGTATAATTG	GAAAACCCAT	660
AATCCTCCCT	TCTCTGAAAA	GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	720
ACACATTGGC	CCACCTGGGA	TGACTGTCAA	CAGCTCCTTT	TGACCCTTTT	CACCTCTGAA	780
GAGAGGGAAA	GTATCCAAAAG	AGAGGCCAAA	AAGTACAACC	TCACATCAAC	CAATAGGCCG	840
GAGGAGGAAG	CTAGAGGAAT	AGTGATTAGA	GACCCAATTG	GGACCTAATT	GGGACCCAAA	900
TTTCTCAAGT	GGAGGGAGAA	CTTTTGACGA	TTTCCACCGG	TATCTCCTCG	TGGGTATTCA	960
GGGAGCTGCT	CAGAAACCTA	TAAACTTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	1020
TGAGTCACCA	GGAGTGT TTT	TAGAGCACCT	CCAGGAGGCT	TATCAGATTT	ACACCCCTTT	1080
TGACCTGGCA	CCCCCGAAA	ATAGCCATGC	TCTTAATTTG	GCATTTGTGG	CTCAGGCAGC	1140
CCCAGATAGT	AAAAGGAAAC	TCCAAAAACT	AGAGGGATTT	TGCTGGAATG	AATACCAGTC	1200
AGCTTTTAGA	GATAGCCTAA	AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAAAACAAG	1260
CAGCTCAGGC	AGCTGAAAAA	AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	1320
TAGATCAGCC	TCATTTGACT	TCCCCTCCCA	CATGGTGTTT	AAATCCAGCT	ACACTACTTC	1380
CTGACTCAAA	CTCCACTATT	CCTGTTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	1440
CTGGCCGACC	TGATCTTCAA	AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	ATGTTCAACAG	1500
ACAGTAGCAG	CTTCCTCGAG	AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	1560
CAGATGTGTT	GTGGGCTCAG	GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	1620
TCGCCCTCAC	TCAGGCTCTC	CGATGGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	1680
ACGCCTTTGC	TACTGTGCAT	GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	1740
CAGCAGGTGG	CTGTAATCCA	CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCGT	1800
GGTAACCAGA	AAGCTGATTC	AGCAGCTCAA	GATGCAGTGT	GACTTTTCAGT	CACGCCTCTA	1860
AACTTGCTGC	CCACAGTCTC	CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	1920
ACAGAAGAAG	AAAAGTGGCC	TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	1980
TTCTTCCTGA	CTCTAGAATC	TTCATACCCC	GAACTCTTGG	GAAAACTTTA	ATCAGTCACC	2040
TACAGTCTAC	CACCCATTTA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	2100
AGATCCCCCA	TCTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGACAA	ACCTGCGCCC	2160
AGGTAAATGC	CAAAAAAGGT	CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	2220
CAGGAGAAAA	GTGGGAAATT	GACTTTACAG	AAGTAAACC	ACACCGGGCT	GGGTACAAAT	2280
ACCTTCTAGT	ACTGGTAGAC	ACCTTCTCTG	GATGGACTGA	AGCATTTGCT	ACCAAAAACG	2340
AAACTGTCAA	TATGGTAGTT	AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CATGGGCTGC	2400
CTGTTTGCCA	TAGGGTCTGA	TAATGGACCG	GCCTTCGCCT	TGTCTATAGT	TTAGTCAGTC	2460
AGTAAGGCGT	TAAACATTCA	ATGGAAGCTC	CATTGTGCCT	ATCGACCCCA	GAGCTCTGGG	2520
CAAGTAGAAC	GCATGAAGTG	CACCCTAAAA	AACACTCTTA	CAAAATTAAT	CTTAGAAACC	2580
GGTGTAATTT	GTGTAAGTCT	CCTTCCTTTA	GCCCTACTTA	GAGTAAGGTG	CACCCCTTAC	2640
TGGGCTGGGT	TCTTACCTTT	TGAAATCATG	TATGGGAGGG	TGCTGCCTAT	CTTGCCTAAG	2700
CTAAGAGATG	CCCAATTGGC	AAAAATATCA	CAAACTAATT	TATTACAGTA	CCTACAGTCT	2760
CCCCAACAGG	TACAAGATAT	CATCCTGCCA	CTTGTTTCGAG	GAACCCATCC	CAATCCAATT	2820
CCTGAACAGA	CAGGGCCCTG	CCATTCAATC	CCGCCAGGTG	ACCTGTTGTT	TGTTAAAAAG	2880
TTCCAGAGAG	AAGGACTCCC	TCCTGCTTGG	AAGAGACCTC	ACACCGTCAT	CACGATGCCA	2940
ACGGCTCTGA	AGGTGGATGG	CATTCTGCG	TGGATTTCATC	ACTCCCGCAT	CAAAAAGGCC	3000
AACAGAGCCC	AAGTAGAAAC	ATGGGTCCCC	AGGGCTGGGT	CAGGCCCTTT	AAAAC'TGCAC	3060
CTAAGTTGGG	TGAAGCCATT	AGATTAATTC	TTTTTCTTAA	TTTTGTAAAA	CAATGCATAG	3120
CTTCTGTCAA	ACTTATGTAT	CTTAAGACTC	AATATAACCC	CCTTGTTATA	ACTGAGGAAT	3180
CAATGATTTG	ATTCCTCCAA	AAACACAAGT	GGGGAATGTA	GTGTCCAACC	TGGTTTTTAC	3240
TAACCCTGTT	TTTAGACTCT	CCCTTTCCTT	TAATCACTCA	GCTTGTTTCC	ACCTGAATTG	3300
ACTCTCCCTT	AGCTAAGAGC	GCCAGATGGA	CTCCATCTTG	GCTCTTTCAC	TGGCAGCCGC	3360
TTCTCAAGG	ACTTAACTTG	TGCAAGCTGA	CTCCCAGCAC	ATCCAAGAAT	GCAATTAAC	3420
GATAAGATAC	TGTGGCAAGC	TATATCCGCA	GTTCCAGGA	ATTCGTCCAA	TTGATCACAG	3480

CCCCTCTACC	CTTCAGCAAC	CACCACCCTG	ATCAGTCAGC	AGCCATCAGC	ACCGAGGCAA	3540
GGCCCTCCAC	CAGCAAAAAG	ATTCTGACTC	ACTGAAGACT	TGGATGATCA	TTAGTATTTT	3600
TAGCAGTAAA	GTTTTTTTTT	CTTTTCTTTT	CTTTTTTTCT	CGTGCC		3646

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TAAGAGGGTA	CAAGATCTAA	GCACAGCCGT	CAATGCAGAA	CACAGAACGT	AGCCTGGTAA	60
GTGTGTAAAG	AGTGGGAATT	TTTGGAGTAC	AGAGTAAGGC	ACCTAACCCT	AGCTGGGGTT	120
TGGTGACGGT	CCCAGATGGC	TTACAGAAGA	AAGTGTCTCTG	AGATGAGTTT	TTAAGAATGA	180
ATAAGGATAG	ACACAAGTGA	GGACTGACTT	GGCAGTGGTG	AATGGTGGGT	GGCAAAAAAC	240
TTTCGCATGTA	TGGAAACTGC	ACGTACAGGA	ATGAAGAATG	AGACTGTGTG	GTGTTTAATG	300
AGCTGCAAAT	ACTAATTTTA	TCCTGAAAGT	TTTGAAGAGT	TAACTAAAAA	GTATTTTSTA	360
GTAAGGAAAT	AACCCTACAT	TTCAGGGTTA	TTGTTTGTTT	ANATATTGAA	GGTGCCCAA	419

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AAGAGGGTAC	CTGTATGTAG	CCATGGTGGC	AATGAGAGAC	TGATTACTAC	CTGCTGGAGA	60
TTGTTTAAAGT	GAGTTAATAT	ATTAAGGATA	AAGGGAGCCA	GGTTTTTTGA	CTGTTGGAGA	120
AGGAAATTAC	AGATATTGAA	GGTCCCAA				148

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TAAGAGGGTA CMAAAAAAAAA AAAATAGAAC GAATGAGTAA GACCTACTAT TTGATAGTAC	60
AACAGGGTGA CTATAGTCAA TGATAACTTA ATTATACATT TAACATAGAG TGTAATTGGA	120
TTGTTTGTA CTCGAAGGAT AAATGCTTGA GAGGATGGAT ACCCCATTCT CCATGATGTA	180
CTTATTTTAC ATTACATGCC TGTATCAAAG CATCTCATAT ACCCTATAAA TATGTACACC	240
TACTATGTAC CCTCTTA	257

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TAAGAGGGTA CGGGTATTTG CTGATGGGAT TTTTTTTTCT TTCTTTTCT TTGGAAAACA	60
AAATGAAAGC CAGAACAAAA TTATTGAACA AAAGACAGGG ACTAAATCTG GAGAAATGAA	120
GTCCCTCAC CTGACTGCCA TTTCATTCTA TCTGACCTTC CAGTCTAGGT TAGGAGAATA	180
GGGGGTGGAG GGGATTAATC TGATACAGGT ATATTTAAAG CAACTCTGCA TGTGTGCCAG	240
AAGTCCATGG TACCCTCTTA	260

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TGCTCCTCTT GCCTTACCAA CCACAAATTA GAACCATAAT GAGATGTCAC CTCATACCTG	60
GTGGGATTAA CATTATTTAA AAAATCAGAA GTATTGACAA GGATGTGAAG AAATTAGAAC	120
ATCTGTGCAC TGTTGGTGGG AATGTAAAAA AGGTGTGGCC ACTATGGGTA ACAGCATGAA	180
GGTTCCTCAA AAAAAATTTT TTTTAATCTA CTCTATGATC GATCTTGAGG TTGTTTATGC	240
AAAAGAACTG AAATCAGGAT TTTGAGGAAA TATTCACATT CCCACATCCA TTTCTGCTTT	300
ATTCATAATA CTCAAGAGAT GGAAACAACC TAAATGTCCA TCCCGGGATG AATGGATAAA	360
CACAGTGTGG TATATGCATA CAATGGAATA TTATTTAGTC TTAAAAAGA AAAATTCTAT	420

CATATACTAC AACTTANATN AACCTTGAGG ACACAATGCT NAGTGAAATA AGCCACGGAA	480
GGACGAATAC TGCATTATTC CCTTATATGA AGTATCTAAA GTGGTCAAAC TCTTANAGCA	540
NAAAGTAAAA ATGGGTGGTT GCCANACAGT TGGTTAGGCN AGAAGANAAN CCTANT	596

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TCTTCTGAAG ACCTTTCGCG ACTCTTAAGC TCGTGGTTGG TAAGGCAAGA GGAGCGTTGG	60
TAAGGCAAGA GGAGCGTTGG TAAGGCAAGA GGAGCA	96

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGTAAGTCGA GCAGTGTGAT GATAAACTT GAATGGATCA ATAGTTGCTT CTTATGGATG	60
AGCAAAGAAA GTAGTTTCTT GTGATGGAAT CTGCTCCTGG CAAAATGCT GTGAACGTTG	120
TTGAAAAGAC AACAAAGAGT TTAGAGTAGT ACATAAATTT AGAATAGTAC ATAACTTAG	180
AATAGTACAT AACTTAGTA CATAAATAAT GCACGAAGCA GGGGCAGGGC TTGAGAGAAT	240
TGACTTCAAT TTGGAAAGAG TATCTACTGT AGGTTAGATG CTCTCAAACA GCATCACACT	300
GCTCGACTTA CAA	313

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AACGAGGACA GATCCTTAAA AAGAATGTTG AGTGAAAAAA GTAGAAAATA AGATAATCTC	60
CAAAGTCCAG TAGCATTATT TAAACATTTT TAAAAAATAC ACTGATAAAA ATTTTGTACA	120
TTTCCCAAAA ATACATATGG AAGCACAGCA GCATGAATGC CTATGGGRTT GAGGATAGGG	180
GTTGGGAGTA GGGATGGGGA TAAAGGGGGA AAATAAAACC AGAGAGGAGT CTTACACATT	240
TCATGAACCA AGGAGTATAA TTATTTCAAC TATTTGTACC WGAAGTCCAG AAAGAGTGGA	300
GGCAGAAGGG GGAGAAGAGG GCGAAGAAAC GTTTTGGGGA GAGGGGTCCC ASAAGAGAGA	360
TTTTCGCGAT GTGGCGCTAC ATACGTTTTT CCAGGATGCC TTAAGCTCTG CACCCTATTT	420
TTCTCATCAC TAATATTAGA TTAAACCCTT TGAAGACAGC GTCTGTGGTT TCTCTACTTC	480
AGCTTTCCCT CCGTGTCTTG CACACAGTAG CTGTTTTACA AGGGTTGAAC TGAAGTGAAGT	540
GAGATTATTC	550

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TAGACTGACT CATGTCCCCT ACCAGAGTAG CTAGAATTAA TAGCACAAGC CTCTACACCC	60
AGGAACTCAC TATTGAATAC ATAAATGGAA TTTATTCAGC CTTAAAAAGT TTGGAAGGAA	120
ATTCTGACAT ATGCTAAAAC ATGGATGAAC CTTGAAGACT TTATGATAAG TAAAAGAAGC	180
CAGTCATAAA AGGAAAAATA TTGCATGATT CCACTTATAT GAGGTACCTA GAGTAGTCAA	240
TTTCATAGAA ACACAAAATA GAATGGTGTT TGCCAGGGCT TTTGAGGAAA AGGGAATGAC	300
AAGTTAGGGG ACATGAGTCA GTCTA	325

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TAGACTGACT CATGTCCCCT ATCTACTCAA CATTTCCACT TGAAGTCTGA TAGGCATCTC	60
AGACTTATCT TGTCCCAAAG CAAACTCTTT ATTTCTTTTC ATCCTAGTCT TTATTTCTTG	120
TGCTGTCTTA CCCATCTCAA AAGAGTGCCA AAATCCACCA AGTTGCTGAA ACAGAAATCT	180

AAGAAATATC CTTGATTCTT CTTTTTCCCA TCTACTTCAC TTCTAATTCA TTAGTAAATA	240
ATCTGTTTTCA GAAAACCAAA CACCTCATGT TCTCACTCAT AAGGGGGAGT TGAACAATGA	300
GAACACACAG ACACAGGGAG GGGAACATCA CACACCACGG CCCGTCAGGG AGTANGGGAC	360
ATGAGTCAGT CTA	373

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TAGACTGACT CATGTCCCCT ATAATGCTCC CAGGCATCAG AAAGCATCTC AAAGTGGAGC	60
TGACACCATG GCAGAGGTTT CAGGTAAGTC ACAAAGGGG TCCTAAAGAA TTTGCCCTCA	120
ATATCAGAGT GATTAGAAGA AGTGGACAGA GCTACCCAAG TTAAACATAT GCGAGATAAA	180
AAAAATATGG CACTTGTGAA CACACACTAC AGGAGGAAAA TAAGGAACAT AATAGCATAT	240
TGTGCTATTA TGATGATGAA GAACCTCTCT ANAAGAAAAC ATAACCAAAG AAACAAAGAA	300
AATTCCTGCN AATGTTTAAT GCTATAGAAG AAATTAACAA AACATATAT TCAATGAATT	360
CAGAAAAGTT AGCAGGTCAN AAGAAAACAA ATCAAAGACC AGAATAATCC CATTTTAGAT	420
TGTCGAGTAA ACTANAACAG AAAGAATACC ACTGGAAATT GAATTCCTAC GTANGGGACA	480
TGANTCANTC TA	492

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TGGAAAGTAT TTAATGATGG GCAACTTGCT GTTTACTTCC TACATATCCC ATCATCTTCT	60
GTATTTTTTT AAATAACTTT TTTTGGATT TTAAAGTAA CCTTATTCTG AGAGGTAACA	120
TGGATTACAT ACTTCTAAGC CATTAGGAGA CTCTATGTTA AACCAAAAGG AAATGTTACT	180
AGATCTTCAT TTGATCAATA GGATGTGATA ATCATCATCT TTCTGCTCTA ATGGAAAAGT	240
ACTANAAACA TGGAACCATA ATCTTAGATG AACAACGTTA GAATTTGCAC TAATTCTACG	300
GAATTTTCAGT AATTCGGCAA ATGTCGGGCA GTGACACAAC ATTTTCATGAC GGGGACGCAT	360
CTACCAACTT CTGGCGATAA GGGCCACCCT TCCCTCTGTA CTTACAGTCC CATTTCATAC	420
ACAGTCTTTG ATTAAATATT CACATTTTTT CTCTACCTAA AGACCTTCAA GACCAGTACG	480
TA	482

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGTATCGACG	TAGTGGTCTC	CCCATGTGAT	AGTCTGAAAT	ATAGCCTCAT	GGGATGAGAG	60
GCTGTGCCCC	AGCCCCGACAC	CCGTAAAGGG	TCTGTGCTGA	GGTGGATTAG	TAAAAGAGGA	120
AAGCCTTGCA	GTTGAGATAG	AGGAAGGGCA	CTGTCTCCTG	CCTGCCCCCTG	GGAAGTGAAT	180
GTCTCGGTAT	AAAACCCGAT	TGTACATTG	TTCAATTCTG	AGATAGGAGA	AAAACCACCC	240
TATGGCGGGA	GGCGAGACAT	GTTGGCAGCA	ATGCTGCCTT	GTTATGCTTT	ACTCCACAGA	300
TGTTTGGGCG	GAGGGAAACA	TAAATCTGGC	CTACGTGCAC	ATCCAGGCAT	AGTACCTCCC	360
TTTGAACCTA	ATTATGACAC	AGATTCCCTT	GCTCACATGT	TTTTTTGCTG	ACCTTCTCCT	420
TATTATCACC	CTGCTCTCCT	ACCGCATTCC	TTGTGCTGAG	ATAATGAAAA	TAATATCAAT	480
AAAAACTTGA	NGGAACTCGG	AGACCACTAC	GTCGATACA			519

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TGTATCGACG	TAGTGGTCTC	CACTCCCGCC	TTGACGGGGC	TGCTATCTGC	CTTCCAGGCC	60
ACTGTCACGG	CTCCCGGGTA	GAAGTCACTT	ATGAGACACA	CCAGTGTTGGC	CTTGTTGGCT	120
TGAAGCTCCT	CAGAGGAGGG	TGGGAACAGA	GTGACCGAGG	GGGCAGCCTT	GGGCTGACCT	180
AGGACGGTCA	GCTTGGTCCC	TCCGCCAAAC	ACGAGAGTGC	TGCTGCTTGT	ATATGAGCTG	240
CAGTAATAAT	CAGCCTCGTC	CTCAGCCTGG	AGCCCAGAGA	TGGTCAGGGA	GGCCGTGTTG	300
CCANACTTGG	AGCCAGAGAA	GCGATTAGAA	ACCCCTGAGG	GCCGATTACC	GACCTCATAA	360
ATCATGAATT	TGGGGGCTTT	GCCTGGGTGC	TGTTGGTACC	ANGAGACATT	ATTATAACCA	420
CCAACGTCAC	TGCTGGTTCC	ANTGCAGGGA	AAATGGTTGA	TCNAACTGTC	CAAGAAAACC	480
ACTACGTCCA	TACCAATCCA	CTAATTGCCN	GCCGCCTGCA	GGTTCAACCA	TATTGGGGAA	540
NAACTCCCN	CCGCCGTTTG	GGATTGNCAT	NAACCTTTGA	AATTTTTTCC	TATTANTTGT	600
CCCCCTAAAA	TAAACCNTTG	GGCNTTAATC	CATTGGGTCC	ATANCTTNTT	TNCCCGGTTT	660
TTAAAANTTG	TTTATCCCGC	CNCCCNATTT	CCCCCCCAAC	TTTCCAAAAC	CCGAAACCNT	720
TNAAATTTNT	TNAAACCCTG	GGGGGTTCCT	NNAATTNNAN	TTNAANCTNC	C	771

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TGGGCACCTT CAATATCGGG CTCATCGATA ACATCAGCT GCTGATGCTG CTGTTGCTGG	60
TCCTCTCTAG GAACCTCTGG ATTTTCAAAT TCTTTGAGGA ATTCATCCAA ATTATCTGCC	120
TCTCCTCCTT TCCTCCTTTT TCTAAGGTCT TCTGGTACAA GCGGTCA	167

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TTGGGCACCT TCAATATCTA CTGATCTAAA TAGTGTGGTT TGAGGCCTCT TGTTCCTGGC	60
TAAAAATCCT TGGCAAGAGT CAATCTCCAC TTTACAATAG AGGTAAAAAT CTTACAATGG	120
ATATTCTTGA CAAAGCTAGC ATAGAGACAG CAATTTTACA CAAGGTATTT TTCACCTGTT	180
TAATAACAGT GGTTTTCCTA CACCCATAGG GTGCCACCAA GGGAGGAGTG CACAGTTGCA	240
GAAACAAATT AAGATACTGA AGACAACACT ACTTACCATT TCCCGTATAG CTAACCACCA	300
GTTCAACTGT ACATGTATGT TCTTATGGGC AATCAAGA	338

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

120

TTTTTGGCTC CCATACAGCA CACTCTCATG GGAAATGTCT GTTCTAAGGT CAACCCATAA	60
TGCAAAAATC ATCAATATAC TTGAAGATCC CCGTGTAAGG TACAATGTAT TTAATATTAT	120
CACTGATACA ATTGATCCAA TACCAGTTTT AGTCTGGCAT TGAATCAAAT CACTGTTTTT	180
GTTGTATAAA AAGAGAAATA TTTAGCTTAT ATTTAAGTAC CATATTGTAA GAAAAAAGAT	240
GCTTATCTTT ACATGCTAAA ATCATGATCT GTACATTGGT GCAGTGAATA TTACTGTAAA	300
AGGGAAGAAG GAATGAAGAC GAGCTAAGGA TATTGAAGGT GCCCAA	346

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

ACCAATCCCA CACGGATACT GAGGGACAAG TATATCATCC CATTTTCATCC CTACAGCAGC	60
AACTTCATGA GGCAGGAGTT ATTAGTCCCA TTTTACAGAA GAGGAAACTG AGACTTAGGG	120
AGATCAAGTA ATTTGCCCAG GTCGCACAAT TAGTGATAGA GCCAGGGCTT GAAGCGACGT	180
CTGTCTTAAG CCAATGACCC CTGCAGATTA TTAGAGCAAC TGTCTCCAC AACAGTGTA	240
GCCTCTTGCT ANAAGCTCAG GTCCACAAGG GCAGAGATTT TTGTCTGTTT TGCTCATTGC	300
TCCTTCCCCA TTGCTTAGAG CAGGGTCTGC CACGAANCAG GTTCTCAATG CATAGTTATT	360
AAATGTATAT AAGAGCAAAC ATATGTTACA GAGAACTTTC TGTATGCTTG TCACTTACAT	420
GAATCACCTG TGANATGGGT ATGCTTGTTT CCCANTGTTG CAGATNAAGA TATTGAANGT	480
GCCCAAATCA CTANTTGGCG GCGCCTGCAN GTCCANCATA T	521

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

TGGAACCAAT CCAAATACCC ATCAATGATA GACTGGATAA AGAAAATTTG GCACATGTTC	60
ACCATGAAAT ACTATGCAGC CATAAAAAAG GATGAGTTCA TATCCTTTGC AGGGACATGG	120
ATGAAGCTGG AGACCATCAT TCTCAGCAAA CTAACAAGGG AACAGAAAAC CAAACACTGC	180
ATGTTCTCAC TCTTAAGTGG GAGCTGAACA ATGAGAACAC ATGGACACAG GGAGGGGAAC	240
ATCACACAGT GGGGCCTGCT GGTGGGTAGG GGTCTAGGGG AGGGATAGCA TTAGGAGAAA	300
TACCTAATGT AGATGACGGG TTGATGGGTG CAGCAAACCA CCATGACACG TGTATACCTA	360
TGTAACAAAC CTGCATGTTT TGCACATGTA CCCCAGAACT TAAAGTGTTA ATAAAAAAT	420
TAAGAAAAAA GTTAAGTATG TCATAGATAC ATAAAAATATT GTANATATTG AAGGTGCCCA	480

AA

482

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTCGATACAG GCACAGAGTA AGCAGAAAAA TGGCTGTGGT TTAACCAAGT GAGTACAGTT	60
AAGTGAGAGA GGGGCAGAGA AGACAAGGGC ATATGCAGGG GGTGATTATA ACAGGTGGTT	120
GTGCTGGGAA GTGAGGGTAC TCGGGGATGA GGAACAGTGA AAAAGTGGCA AAAAGTGGTA	180
AGATCAGTGA ATTGTACTTC TCCAGAATTT GATTTCTGGN GGAGTCAAAT AACTATCCAG	240
TTTGGGGTAT CATANGGCAA CAGTTGAGGT ATAGGAGGTA GAAGTCNCAG TGGGATAATT	300
GAGGTTATGA ANGGTTTGGT ACTGACTGGT ACTGACAANG TCTGGGTTAT GACCATGGGA	360
ATGAATGACT GTANAAGCGT ANAGGATGAA ACTATTCCAC GANAAAGGGG TCCNAAAAC	420
AAAAANNNA GNNNNNGGG AATATTATTT ATGTGGATAT TGAANGTGCC CAAA	474

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANACG GTGCTTACGT CCTTTTGCTC TGTTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG	240
TTCCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTCAACAGTT TCCGATGGCT GTGATGGGCA TAGTCATANT TAACNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGATTGGT CCTCCAGGAG AACAAAGGGGA AAAAGGTGAC CGAGGGCTCC CTGGAAC	60
AGGATCTCCA GGAGCAAAAG GGGATGGGGG AATTCCTGGT CCTGCTGGTC CCTTAGG	120

ACCTGGTCCT	CCAGGCTTAC	CAGGTCCTCA	AGGCCCAAAG	GGTAACAAAG	GCTCTACTGG	180
ACCCGCTGGC	CAGAAAGGTG	ACAGTGGTCT	TCCAGGGCCT	CCTGGGCCTC	CAGGTCCACC	240
TGGTGAAGTC	ATTGAGCCTT	TACCAATCTT	GTCTCTCCAA	AAAACGAGAA	GACATACTGA	300
AGGCATGCAA	GCAGATGCAG	ATGATAATAT	TCTTGATTAC	TCGGATGGAA	TGGAAGAAAT	360
ATTTGGTTCC	CTCAATTCCC	TGAAACAAGA	CATCGAGCAT	ATGAAATTTC	CAATGGGTAC	420
TCAGACCAAT	CCAA					434

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGGATTGGTC	ACATGGCAGA	GACAGGATTC	CAAGGCAGTG	AGAGGAGGAT	ACAATGCTTC	60
TCACTAGTTA	TTATTATTTA	TTTTATTTTT	GAGATGAACT	CTCGCTTTGT	CTCCCAGGCT	120
GGAGAGCGGT	GGTGCGATCT	TGGCTCTCTG	CAACCCCCGC	CTCAAGCAAT	TCTCCTGTCT	180
TAGCCTCGCG	GGTAGATGGA	ATTACAGGCG	CCCACCGCCA	TGCCCAACTA	ATTTTTTTGT	240
GTCTTCAGTA	GAGACAGGGT	TTCGCCATGT	TGGGCAGGCT	GGTCTTGAAC	TCCTGACCTC	300
NAGTGATCTG	CCCTCCTCGG	CCTCACAAAG	TGCTGGAATT	ACAGGCATGG	GCTGCTGCAC	360
CCAGTCAACT	TCTCACTAGT	TATGGCCTTA	TCATTTTCAC	CACATTCTAT	TGGCCCCAAA	420
AAAAAAAAAN						430

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGGTACTCCA	CCATYATGGG	GTCAACCGCC	ATCCTCGCCC	TCCTCCTGGC	TGTTCTCCAA	60
GGAGTCTGTG	CCGAGGTGCA	GCTGRTGCAG	TCTGGAGCAG	AGGTGAAAAA	GTCCGGGGGAG	120
TCTCTGAAGA	TCTCCTGTAA	GGGTCTCTGA	TACACCTTTA	AGATCTACTG	GATCGCCTGG	180
GTGCGCCAGT	TGCCCGGGAA	AGGCCTGGAG	TGGATGGGGC	TCATCTTTCC	TGATGACTCT	240
GATACCAGAT	ACAGCCCGTC	CTTCCAAGGC	CAGGTCACCA	TCTCAGTCGA	TAAGTCCATC	300
AGCACCGCCT	ATCTGCAGTG	GAGTACCAA				329

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TGGTACTCCA	CTCAGCCCCA	CCTTAATTAA	GAATTAAGAG	GGAACCTATT	ACTATTCTCC	60
CAGGCTCCTC	TGCTCTAACC	AGGCTTCTGG	GACAGTATTA	GAAAAGGATG	TCTCAACAAG	120

TATGTAGATC	CTGTACTGGC	CTAAGAAGTT	AAACTGAGAA	TAGCATAAAT	CAGACCAAAC	180
TTAATGGTCG	TTGAGACTTG	TGTCCTGGAG	CAGCTGGGAT	AGGAAAACCT	TTGGGCAGCA	240
AGAGGAAGAA	CTGCCTGGAA	GGGGGCATCA	TGTTAAAAAT	TACAAGGGGA	ACCCACACCA	300
GGCCCCCTTC	CCAGCTCTCA	GCCTAGAGTA	TTAGCATTTT	TCAGCTAGAG	ACTCACAAC	360
TCCTTGCTTA	GAATGTGCCA	CCGGGGGGAG	TCCCTGTGGG	TGATGAGGCT	CTCAAGAGTG	420
AGAGTGGCAT	CCTATCTTCT	GTGTGCCAC	AGGAGCCTGG	CCCAGACTT	AGCAGGTGAA	480
GTTTCTGGTC	CAGGCTTTGC	CCTTGACTCA	CTATGTGACC	TCTGGTGGAG	TACCAA	536

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

NTGTTGCGAT	CCCAGTAACT	CGGGAAGCTG	AGGCGGGAGG	ATCACCTGAG	CTCAGGAGGT	60
TGAGGCCGCA	GTGAGCCGGG	ACCACGCCAC	TACACTCCAG	CCTGGGGCAT	AGAGTGAGAC	120
CCTCCAAGAC	AGAAAAGAAA	AGAAAGGAAG	GGAAAGGGAA	ACGGAAAAGG	AAAAGGAAAA	180
GGAAAAGGAA	AAGGAAAAGA	CAAGACAAAA	CAAGACTTGA	ATTTGGATCT	CCTGACTTCA	240
ATTTTATGTT	CTTTCTACAC	CACAATTCCT	CTGCTTACTA	AGATGATAAT	TTAGAAACCC	300
CTCGTTCCAT	TCTTTACAGC	AAGCTGGAAG	TTTGGTCAAG	TAATTACAAT	AATAGTAACA	360
AATTTGAATA	TTATATGCCA	GGTGTTTTTC	ATTCTGCTC	TCACTTAATT	CTCACCCTC	420
TGATATAAAT	ACAATTGCTG	CCGGGTGTGG	TGGCTCATGC	CTGTAATCCC	GGCACTTTGG	480
GAGACCGAGG	TGGGCGGATS	GCAACAA				507

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TTGGATTGGT	CACTGTGAGG	AAGCCAAATC	GGATCCGAGA	GTCTTTTCT	AAAGGCCAGT	60
ACTGGCCACA	CTTTCTCCTG	CCGCCTTCCT	CAAAGCTGAA	GACACACAGA	GCAAGGCGCT	120
TCTGTTTTAC	TCCCCAATGG	TAACTCCAAA	CCATAGATGG	TTAGCTNCCC	TGCTCATCTT	180
TCCACATCCC	TGCTATTGAG	TATAGTCCGT	GGACCAATCC	AA		222

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TGTTGCGATC	CATAAATGCT	GAAATGGAAA	TAAACAACAT	GATGAGGGAG	GATTAAGTTG	60
GGGAGGGAGC	ACATTAAGGT	GGCCATGAAG	TTTGTGGAA	GAAGTGA	TTGAACAAGG	120

CCTTGGTGTT AAGAGCTGAT GAGAGTGTCC CAGACAGAGG GGCCACTGGT ACAATAGACG	180
AGATGGGAGA GGGCTTGGAA GGTGTGCGAA ATAGGAAGGA GTTGTTCCTG GTATGAGTCT	240
AGTGAACACA GAGGCGAGAG GCCCTGGTGG GTGCAGCTGG AGAGTTATGC AGAATAACAT	300
TAGGCCCTGT GGGGGACTGT AGACTGTCAG CAATAATCCA CAGTTTGGAT TTTATTCTAA	360
GAGTGATGGG AAGCCGTGGA AAGGGGGTTA AGCAAGGAGT GAAATTATCA GATTACAGT	420
GATAAAAATA AATTGGTCTG GCTACTGGGG AAAAAAAAAA AAA	463

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

TTGGATTGGT CAACCTGCTC AACTCTACYT TTCCTCCTTC TTCCTAAAAA ATTAATGAAT	60
CCAATACATT AATGCCAAAA CCCTTGGGTT TTATCAATAT TTCTGTAAAA AAGTATTATC	120
CAGAACTGGA CATAATACTA CATAATAATA CATAACAACC CCTTCATCTG GATGCAAACA	180
TCTATTAATA TAGCTTAAGA TCACTTTCAC TTTACAGAAG CAACATCCTG TTGATGTTAT	240
TTTGATGTTT GGACCAATCC AA	262

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GNGGNNNNNN NNNCAATTCG ACTCNGTTCC CNTGGTANCC GGTGACATG GCCGCGGGAT	60
TACCGCTTGT NNCTGGGGGT GTATGGGGGA CTATGACCGC TTGTAGCTGG GGGTGTATGG	120
GGGACTATGA CCGCTTGTAG MTGGKGGTGT ATGGGGGACT ATGACCGCTT GTCGGGTGGT	180
CGGATAAACC GACGCAAGGG ACGTGATCGA AGCTGCGTTC CCGCTCTTTC GCATCGGTAG	240
GGATCATGGA CAGCAATATC CGCATTCGYC TGAAGGCGTT CGACCATCGC GTGCTCGATC	300
AGGCGACCGG CGACATCGCC GACACCGCAC GCCGTACCGG CGCGCTCATC CGCGGTCCGA	360
TCCCGCTTCC CACGCGCATC GAGAAGTTCA CGGTCAACCG TGGCCCGCAC GTCGACAAGA	420
AGTCGCGCGA GCAGTTCGAG GTGCGTACCT ACAAGCGGTC A	461

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TGACCGCTTG TAGCTGGGGG TGTATGGGGG ACTACGACCG CTTGTAGCTG GGGGTGTATG	60
GGGACTATG ACCGCTTGTA GCTGGGGGTG TATGGGGGAC TATGACCGCT TGTAGCTGGG	120
GGTGTATGGG GGACTAGGAC CGCTTGTAGC TGGGGGTGTA TGGGGGACTA TGACCGCTTG	180

TAGCTGGGGG TGTATGGGGG ACTACGACCG CTTGTAGCTG GGGGTGTATG GGGGACTATG	240
ACCGCTTGTA NCTGGGGGTG TATGGGGGAC TATGACCGCT TGTGCTGCCT GGGGGATGGG	300
AGGAGAGTTG TGTTGGGGA AAAAAAAAAA AA	332

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT	60
GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT	120
GACCGCTTGT GACCGCTTGT NACNGGGGGT GTCTGGGGGA CTATGANNGA NTGTNACTGG	180
GGGTGTCTGG GGGNCTATGA NNGANTGTNA CNGGGGGTGT CTGGGGGACT ATGANNGACT	240
GTGCNNCTG GGGGATCNGA GGAGANTNGN GGNTAGNGAT GGTNNGGAN A	291

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

TAAGAGGGTA CTGGTTAAAA TACAGGAAAT CTGGGGTAAT GAGGCAGAGA ACCAGGATAC	60
TTTGAGGTCA GGGATGAAAA CTAGAATTTT TTTCTTTTTT TTTGCCTGAG AAACCTTGCTG	120
CTCTGAAGAG GCCCATGTAT TAATTGCTTT GATCTTCCTT TTCTTACAGC CCTTCAAGG	180
GCAGAGCCCT CTTATCCTG AAGGAATCTT ATCCTTAGCT ATAGTATGTA CCCTCTTA	238

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TTGGGCACCT TCAATATCAA TAGCTAACAT TTATTGAGTG TTTATCGTAT CATAAAACAC	60
TGTTCTAAGC CTTTAAACGT ACTAATTCAT TTAATGCTCA TAATCACTTT AGAAGGTGGG	120
TACTAGTATT AGTCTCATTT ACAGATGCAA CATGCAGGCA CAGAGAGGTT AATTAAGTTG	180
CCCAAGGTAA CACAGCTAAG AAATAGAAAA AATATTGAAT CTGGAAAGTT GGGCTTCTGG	240
GTAACCCACA GAGTCTTCAA TGAGCCTGGG GCCTCACTCA GTTTGCTTTT ACAAAGCGAA	300
TGAGTAACAT CACTTAATTC AGTGAGTAGG CCAAATGGAG GTCAGCTACG AGTTTCTGCT	360
GTTCTTGCGAG TGGACTGACA GATGTTTACA ACGTCTGGCC ATCAGTWAAT GGACTGATTA	420
TCATTGGGAW GTGGGTGGGC TGAATGTTGG CCAAGTGAAGT TTATTCAWGC CATATTTTTA	480
TGTTTAGGAT GACTTTTGGC TGGTCCTAGG GCAAGCTCTG TCTGSCACGG AACACAGAAT	540
WACACAGGGA CCCCTCAAT TTCTGGTGTG GCTAGAACCA TGAACCACTG GTTGGGGGAA	600

CAAGCGGTCA AAACCTAAGT GCGGCCGGCT GGCAGGGTCC ACCCATATGG GGAAAACTCC	660
CNACGCGTTT GGAATGCCTN AGCTNGAATT ATTCTAANAG TTGTCCNCNT AAAATTAGCC	720
TGGGCGTTAA TCANGGGTCN NAAGCC	746

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TGACCGCTTG TCATCTCACA TGGGGTCCTG CACGCTTTTG CCTTTGTAGG AAACCTGACA	60
TTTGTCTGTT TCTTCTTTCT CTTTTCCTTC CCATATCCTC CTAATTTACG TTTGACTTGT	120
TTGCTGAGGA GGCAGGAGCT AGAGACTGCT GTGAGCTCAT AGGGGTGGGA AGTTTATCCT	180
TCAAGTCCCG CCCACTCATC ACTGCTTCTC ACCTTCCCTT GACCAGGCTT ACAAGTGGGT	240
TCTTGCCCTGC TTTCCCTTTG GACCCAACAA TCCCCTGTAA TGAGTGTGCA TGA CTCTGAC	300
AGCTGTGGAC TCAGGGTCCT TGGCTACAGC TGCCATGTAA AATATCTCAT CCAGTTCTCG	360
CAAATTGTTA AAATAACCAC ATTTCTTAGA TTCCAGTACC CAAATCATGT CTTTACGAAC	420
TGCTCCTCAC ACCCAGAAGT GGCACAATAA TTCTTGGGGA ATTATTACTT TTTTTTTTCT	480
CTCTNTTNNC GNNNGNNNG GNNNGNCCAG GAATTACCAC NTTGGAAGAC CTGGCCNGAA	540
TTTATTATAN AGGGGAGCCG ATTNTTTTTC CTAACACAAA GCGGGTCA	588

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTTTTTTTTT TTTGGCCTGA GCAACTGAAA TTATGAAATT TCCATATACT CAAAAGAGTA	60
AGACTGCAAA AAGATTAAAT GTAAAAGTTG TCTTGTATAC AGTAATGTTT AAGATACCTA	120
TTANATTTAT AAATGGAAAA TTAGGGCATT TGGATATACA AGTTGAAAAT TCAGGAGTGA	180
GGTTGGGCTG GCTGGGTATA TACTGAAAAC TGCAGTACA CAGATGACAT CTAAAACCAC	240
AAATCTGGTT TTATTTTAGC AGTGATATGT GTCACTCCCA CAAAAGCCTT CCAATTGGC	300
CTCAGCATAC ACAACAAGTC ACCTCCCCAC AGCCCTCTAC ACATAAACA ATTCTTAGT	360
TTAGTTCAGG AGGAAATGCG CCCTTTTCCT TCCGCTCTAG GTGACCGCAA GGCCAGTTC	420
TCGTACCAA GATGTTAAGG GAAGTCTGCC AAAGAGGCAT CTGAAAGGAA ATAAGGGGAA	480
TGGGAGTGAC CACAAAGGAA AGCCAAGGAN AAACCTTGGA GACCGTTTCT AGANCCCTGG	540
CATTTACAA CAAAACCTNG GAACAAACCT TGTCTCATCA ATCATTTAAG CCCTTCGTTT	600
GGANNAGACT TTCTGAACTG GGCGCTGAAC ATAANCCTCA TTGAATGTCT TCACAGTCTC	660
CCAGCTGAAG GCACACCTTG GGCCAGAAGG GGAATCTTCC AGGTCCTCAA NACAGGGCTC	720
GCCCTTTGNC	730

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TTTTTTTTTT TTTGGCCAGT ATGATAGTCT CTACCACTAT ATTGAAGCTC TTAGGTCATT	60
TACACTTAAT GTGGTTATAG ATGCTGTTGA GCTTACTTCT ACCACCTTGC TATTTCTCCC	120
GTCTCTTTTT TGTTCCTTTT CTCTTCTTTT CCTCCCTTAT TTTATAATTG AATTTTTTAG	180
GATTCTATTT TATATAGATT TATCAGCTAT AACACTTTGT ATTCTTTTGT TTTGTGGTTC	240
TTCTGTCATT TCAATGTGCA TCTTAAACTC ATCACAATCT ATTTTCAAAT AATATCATAT	300
AACCTTACAT ATAATGTAAG AATCTACCAC CATATATTTT CATTCTCTCCC TTCCATCCTA	360
TGTNTGTCAT ATTTTTTCCT TTATATATGT TTTAAAGACA TAATAGTATA TGGGAGGTTT	420
TTGCTTAAAA TGTGATCAAT ATTCCTTCAA NGAAACGTAA AAATTCAAAA TAAATNTCTG	480
TTTATTCTCA AATNNACCTA ATATTTCCTA CCATNTCTNA TACNTTTCOA GAATCTGAAG	540
GCATTGGTTT TTTCCGGCTT AAGAACCCTC TCTAAAGCAC TCTAAGCAGA ATTAAGTCTT	600
CTGGGAGAGG AATTCTCCCA AGCTTGGGCC TTNANNTGTA CTCCTNANG GTTAAANTTT	660
GGCCGGGAAA TAGAAATTCC AAGTTAACAG GNTANTTTTT NTTTTNTTN TCNCC	715

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TTTTTTTTTT TTTCCCAACA CAAAGCACCA TTATCTTCC TCACAATTTT CAACATAGTT	60
TGATTTCCAT GAAGAGGTTA TGATTTCTAA AGAAAACATG GCTACTATAC TATCAATCAG	120
GGTTAAATCT TTTTTTTT AGACGGAGTT TA	152

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TAAACTCCGT CCCCTTCTTA ATCAATATGG AGGCTACCCA CTCCACATTA CCTTCTTTTC	60
AAGGGACTGT TTCCGTAAC TTTGTGGGTA TTCACGACCA GGCTTCTAAA CCTCTTAAAA	120
CTCCCCAATT CTGGTGCCAA CTTGGACAAC ATGCTTTTTT TTTTTTTTTT TTTTTTTTTN	180
GAGACGGAGT TTA	193

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TGTTGCGATC	CCTTAAGCAT	GGGTGCTATT	AAAAAAATGG	TGGAGAAGAA	AATACCTGGA	60
ATTTACGTCT	TATCTTTAGA	GATTGGGAAG	ACCCTGATGG	AGGACGTGGA	GAACAGCTTC	120
TTCTTGAATG	TCAATTCCTA	AGTAACAACA	GTGTGTCAGG	CACTTGCTAA	GGATCCTAAA	180
TTGCAGCAAG	GCTACAATGC	TATGGGATTC	TCCCAGGGAG	GCCAATTTCT	GAGGGCAGTG	240
GCTCAGAGAT	GCCCTTCACC	TCCCATGATC	AATCTGATCT	CGGTTGGGGG	ACAACATCAA	300
GGTGTTTTTG	GACTCCCTCG	ATGCCCAGGA	GAGAGCTCTC	ACATCTGTGA	CTTCATCCGA	360
AAAACACTGA	ATGCTGGGGC	GTACTCCAAA	GTTGTTTCAGG	AACGCCTCGT	GCAAGCCGAA	420
TACTGGCATG	ACCCATAAAA	GGAGGATGTG	GATCGCAACA			460

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TGTTGCGATC	CGTTGATAGA	ATAGCGACGT	GGTAATGAGT	GCATGGCACG	CCTCCGACTT	60
ACCTTCGCCC	GTGGGGACCC	CGAGTACGTC	TACGGCGTCG	TCACTTAGAG	TACCCCTCTGG	120
ACGCCCCGGG	GCGTTTCGATT	TACCGGAAGC	GCGAGCTGCA	GTGGGCTTGC	GCCCCCGGCC	180
AAATTCCTTT	GGGGGTTTAA	GGCCGCGGGG	AATTTGAGGT	ATCTCTATCA	GTATGTAGCC	240
AAGTTGGAAC	AGTCGCCATT	CCCGAAATCG	CTTCTTTTGA	ATCCGCACCG	CCTCCAGCAT	300
TGCCTCATTC	ATCAACCTGA	AGGCACGCAT	AAGTGACGGT	TGTGTCTTCA	GCAGCTCCAC	360
TCCATAACTA	GCGCGCTCGA	CCTCGTCTTC	GTACGCGCCA	GGTCCGTGCG	TGCGAATTCC	420
CAACTCCGGT	GAGTTGCGCA	TTTCAAGTTN	CGAAACTGTT	CGCCTCCACN	ATTTGGCATG	480
TTCACGCATG	ACACGGAATA	AACTCGTCCA	GTACCGGGAA	TGGGATCGCA	ACA	533

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTTTTTTTTT	TTGCGCTGAA	TTAGCTACAG	ATCCTCCTCA	CAAGCGGTCA	50
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(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TGTTGCGATC	CAAATAACCC	ACCAGCTTCT	TGCACACTTC	GCAGAAGCCA	CCGTCCTTTG	60
GCTGAGTCAC	GTGAACGGTC	AGTGCAAGCA	GCCGCGTGCC	AGAGCAGAGG	TGCAGCATGC	120
TGCACACCAG	CTCAGGGCTG	ACCTCCTCCA	GCAGGATGGA	CAGGATGGAG	CTGCCGTACG	180

TGTCCACCAC	CTCCTGGCAC	TCTTCCGACA	GGGACTTCGG	CAGCTTCGAG	CACATTTTGT	240
CAAAAGCGTC	GAGTATTTCT	TTCTCAGTCT	TGTTGTTGTC	AATCAGCTTG	GTCACCTCCT	300
TCACCAGGAA	TTACACACACC	TCACAGTAAA	CATCAGACTT	TGCTGGGACC	TCGTGCTTCT	360
TAATGGGCTC	CACCAAGTCC	AGGGCAGGGA	TGACATTCTT	GGAGGCCACT	TTGGCGGGGA	420
CCAGAGTCTG	CATGGGCATC	TCTTTCACCT	CATCACAGAA	CCCAACCAGC	GCACAGATCT	480
CCTTGGGTTG	CATGTGCATC	ATCATCTGGG	ATCGCAACA			519

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TTTTTTTTTT	TTGGGGCGGC	GACCGGACGT	GCACTCCTCC	AGTAGCGGCT	GCACGTCGTG	60
CCAATGGCCC	GCTATGAGGA	GGTGAGCGTG	TCCGGCTTCG	AGGAGTTCCA	CCGGGCCGTG	120
GAACAGCACA	ATGGCAAGAC	CATTTTCGCC	TACTTTACGG	GTTCTAAGGA	CGCCGGGGGG	180
AAAAGCTGGT	GCCCCGACTG	CGTGCAGGCT	GAACCAGTCG	TACGAGAGGG	GCTGAAGCAC	240
ATTAGTGAAG	GATGTGTGTT	CATCTACTGC	CAAGTAGGAG	AAGAGCCTTA	TTGGAAAGAT	300
CCAAATAATG	ACTTCAGAAA	AAACTTGAAA	GTAACAGCAG	TGCCTACACT	ACTTAAGTAT	360
GGAACACCTC	AAAACTGGT	AGAATCTGAG	TGTCTTCAGG	CCAACCTGGT	GGAAATGTTG	420
TTCTCTGAAG	ATTAAGATTT	TAGGATGGCA	ATCAAGA			457

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTTTTTTTTT	TTGGGCAACA	ACCTGAATAC	CTTTTCAAGG	CTCTGGCTTG	GGCTCAAGCC	60
CGCAGGGGAA	ATGCAACTGG	CCAGGTCACA	GGGCAATCAA	GA		102

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTTTTTTTTT	TTGGCAATCA	ACAGGTTTAA	GTCTTCGGCC	GAAGTTAATC	TCGTGTTTTT	60
GGCAATCAAC	AGGTTTAAAGT	CTTCGGCCGA	AGTTAATCTC	GTGTTTTTGG	CAATCAACAG	120
GTTTAAAGTCT	TCGGCCGAAG	TTAATCTCGT	GTTTTTGGCA	ATCAACAGGT	TTAAGTCTTC	180
GGCCGAAGTT	AATCTCGTGT	TTTTGGCAAT	CAACAGGTTT	AAGTCTTCGG	CCGAAGTTAA	240
TCTCGTGTTT	TTGGCAATCA	ACAGGTTTAA	GTCTTCGGCC	GAAGTTAATC	TCGTGTTTTT	300
GGCAATCAAG	AGGTTTAAAGT	CTTCGGCCGA	AGTTAATCTC	GTGTTTTTGG	CAATCAACAG	360

GTTTAAGTCT TCGGCCGAAN TTAATCTCGT GTTTTTGGCA ATCAACAGGT TTAANTCTTC 420
 GGCCGAAGTT AATCTCGTGT TTTTGGCAAT CAANA 455

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

TTTTTTTTTT TTGGCCAATA CCCTTGATGA ACATCAATGT GAAAATCCTC GGTAATAATAC	60
TGGCAAACCA AATCCAGCAG CACATCAAAA AGCTTATCCA CCATGATCAA GTGGGCTTCA	120
TCCCTGGGAT GCAAGGCTGG TTCAACATAA GAAAATCAAT AAATGTAATC CATCACATAA	180
ACAGAACCAA AGACAAAAAC CACATGATTA TCTCAATAGA TGCAGAAAAG GCCTTGGACA	240
AATTCAACAG CCCTTCATGC TAAACACTCT TAATAAACTA GATATTGATG GAATGTATCT	300
CAAAATAATA AGAGCTATTT ATGACAAACC CACAGCCAAT ATCATACTGA ATGGGCAAAG	360
ACTGGAAGCA TTCCCTTTGA AAAGTGGCAC AAGACAAGGA TGCCCTCTCT CACCGCTCCT	420
ATTCAACATA GTATTGGAAG TTCTGGCCAG GGCAATCAAG A	461

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TTTTTTTTTT TTGGCCAACA CCAAGTCTTC CACGTGGGAG GTTTTATTAT GTTTTACAAC	60
CATGAAAACA TAGGAAGGTG GCTGTTACAG CAAACATTTC AGATAGACGA ATCGGCCAAG	120
CTCCCCAAC CCCACCTTCA CAGCCTCTTC CACACGTCTC CCANAGATTG TTGTCCTTCA	180
CTTGCAAATT CANGGATGTT GGAAGTNGAC ATTTNNAGTN GCNGGAACCC CATCAGTGAA	240
NCANTAAGCA GAANTACGAT GACTTTGANA NACANCTGAT GAAGAACACN CTACNGANAA	300
CCCTTTCTNT CGTGTTANGA TCTCNNGTCC NTCATAATG CGGCCCCCTG CNGGTCCACC	360
ATTTGGGAGA ACTCCCCCN CGTTGGATCC CCCCTTGAGT NTCCCATTCT NGTCCCCCAN	420
ACCGNCTTG NGNGNCANTN CNNCCTCNCA CCNTGTTTCC CTGNNGTNAA AATNNGTTTT	480
NCCGCCNCCC NAATTCCCAC CCNAATCACA GCGAANCCNG AAGGCCTTCN NAAGTGTTTA	540
ANGCCCNGNG GTTTCCTCNT NTANTTGCA CCTACCCTCC CNCTTNMNNT TNCNGTTGG	600
TCGCGCCCTG GNCNCGCTN GTTCCTCTTT NNGGNNACAA CCTNGNTCNN NGGCNNTCN	660
NNNCTNTTCC TNNNACTAGC TNGCCTNTCC NCNCCGNGGN NCANNGCACA TTNCNCNNAC	720
TNTGTNNCC	729

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

TGACCTGACA	TGTAGTAGAT	ACTTAATAAA	TATTTGTGGA	ATGAATGGAT	GAAGTGGAGT	60
TACAGAGAAA	AATAGAAAAG	TACAAATTGT	TGTCAGTGTT	TTGAAGGAAA	ATTATGATCT	120
TTCCCAAAGT	TCTGACTTCA	TTCTAAGACA	GGGTTAGTAT	CTCCATACAT	AATTTTACTT	180
GCTTTTGAAA	ATCAAATGAG	ATAATCTATT	TAGATTGATA	ATTTATTTAG	ACTGGCTATA	240
AACTATTAAAG	TGCTAGCAAA	TATACATTTT	AATCTCATTT	TCCACCTCTT	GTGATATAGC	300
TATGTAGGTG	TTGACTTTAA	TGGATGTCAG	GTCAATCCC			339

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGACCTGACA	TCCATAACAA	AATCTTTCTC	CATTATATTC	TTCTAGGGGA	ATTTCTTGAA	60
AAGCATCCAA	AGGAAACAAA	TGATGGTAAG	ACCGTGCCAA	GTGGGGAGCA	GACACCAAAG	120
TAAGACCACA	GATTTTACAT	TCAACAGGTA	GCTCACAGTA	CTTTGCCCCG	CATGTGGGC	180
AGAAATAGCC	TCCTAATGTA	AGCCCTGGCT	CAGTATTGCC	ATCCAAATGC	GCCATGCTGA	240
AAGAGGGTTT	TGCATCCTGG	TCAGATNAAG	AAGCAATGGT	GTGCTGAGGA	AATCCCATAC	300
GAATAAGTGA	GCATTCAGAA	CTTGAGCTAG	CAGGAGGAGG	ACTAAGATGA	TGTGTGAGCA	360
ACTCTTTGTA	ATGGCTTTCA	TCTAAAATAA	CATGGTACGT	GCCACCAGTT	TCACGAGCAA	420
GTACAGTGCA	AACGCGAACT	TCTGCAGACA	ATCCAATAAC	AGATACTCTA	ATTTTAGCTG	480
CCTTTAGGGT	CTTGATTAAA	TCATAAATAT	TAGATGGATC	GCAAGTTGTA	AGGNTGCTAA	540
AAGATGATTA	GTACTTCTCG	ACTTGTATGT	CCAGGCATGT	TGTTTTAAAN	TCTGCCTTAG	600
NCCCTGCTTA	GGGGAATTTT	TAAAGAAGAT	GGCTCTCCAT	G TTCANGGTC	AATCACNAAT	660
TGCC						664

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TGACCTGACA	TTGAGGAAGA	GCACACACCT	CTGAAATTCC	TTAGGTTTCAG	AAGGGCATT	60
GACACAGAGT	GGGCCTCTGA	TAATTCATGA	AATGCATTCT	GAAGTCATCC	AGAATGGAGG	120
CTGCAATCTG	CTGTGCTTTG	GGGGTTGCCT	CAGTGTGCTC	CTGGATATCA	CACAAAAGCT	180
GCAATCCTTC	TTCTTCAACT	AACATTTTGC	AGTATTTGCT	GGGATTTT	CTGCAGACAT	240
GATACATAGC	CCATAGTGCC	CAGAGCTGAA	CCTCTGGTTG	AGAGAAGTTG	CCAAGGAGCG	300
GGAAAAATGT	CTTGAAAGAT	CTATAGGTCA	CCAATGCTGT	CATCTTACAA	CTTGAACCTG	360
GCCAATTCTG	TATGGTTGCA	TGCAGATCTT	GGAGAAGAGT	ACGCTCTGG	AAGTCACGGG	420
ATATCCAAAN	CTGTCTGTCA	GATGTCAGGT	CA			452

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TTTTTTTTTTT TTCGGCAAGG CAAATTTACT TCTGCAAAAG GGTGCTGCTT GCACTTTTGG	60
CCACTGCGAG AGCACACCAA ACAAAGTAGG GAAGGGGTTT TTATCCCTAA CGCGGTTATT	120
CCCTGGTTCT GTGTCGTGTC CCCATTGGCT GGAGTCAGAC TGCACAATCT ACACTGACCC	180
AACTGGCTAC TGTTTAAAT TGAATATGAA TAATTAGGTA GGAAGGGGGA GGCTGTTTGT	240
TACGGTACAA GACGTGTTT GGCATGTCAG GTCA	274

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TACCTGACAT GGAGAAATAA CTTGTAGTAT TTTGCGTGCA ATGGAATACT ATATGAGGGT	60
GAAAATGAAT GAACTAGCAA TGCCTGTATC AACATGAATA AATCCCCAAA ACATAATAAT	120
GTTGAATGGA AAAGGTGAGT TTCAGAAGGA TATATATGCC CTCTAAATCC ATTTATGTAA	180
ACCTTTAAAA AACTACATTA TTTATGGTCA TAAGTCCATC CAGAAAATAT TAAAAACCT	240
ACATGGGATT GATAACTACT GATGTCAGGT CA	272

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

TTTTTTTTTTT TTGGCCAATA GCATGATTTA AACATTGGAA AAAGTCAAAT GAGCAATGCG	60
AATTTTTTATG TTCTCTTGAA TAATCAAAAG AGTAGGCAAC ATTGGTTCCT CATTCTTGAA	120
TAGCATTAAAT CAGAAAATAT TGCATAGCCT CTAGCCTCCT TAGAGTAGGT GTGCTCTCTC	180
AAATATATCA TAGTCCCACA GTTTATTTCA TGTATATTTT CTGCCTGAAT CACATAGACA	240
TTTGAATTTG CAACGCCTGA TGTAATATA TAAATTCTTA CCAATCAGAA ACATAGCAAG	300
AAATTCAGGG ACTTGATCAT YATCAGGGTA TGACAGCANA TCCCTGTARA AACACTGATA	360
CACACTCACA CACGTATGCA ACGTGGAGAT GTCGCTTTWW KKKTWYWCWM RMRYCRWCGN	420
AATCACTTAN N	431

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATTCGATTTCG ATGCTTGAGC CCAGGAGTTC AAGACTGCAG TGAGCCACTG CACTTCAGGC 60
 TGGACAACAG AGCGAGTCCC TGTGCCAAAA AAAAAAAAAA 98

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

TTTTTTTTTT	TTCGCAAGCA	CGTGCACTTT	ATTGAATGAC	ACTGTAGACA	GGTGTGTGGG	60
TATAAACTGC	TGTATCTAGG	GGCAGGACCA	AGGGGGCAGG	GGCAACAGCC	CCAGCGTGCA	120
GGGCCASCAT	TGCACAGTGG	ASTGCAAAGG	TTGCAGGCTA	TGGGCGGCTA	CTAVTAACCC	180
CGTTTTTCCT	GTATTATCTG	TAACATAATA	TGGTAGACTG	TCACAGAGCC	GAATWCCART	240
HACASGATGA	ATCCAAWGGT	CAYGAGGATG	CCCASAATCA	GGGCCCASAT	STTCAGGCAC	300
TTGGCGGTGG	GGGCATASGC	CTGKGCCCCG	GTCACGTCSC	CAACCWTCTY	CCTGTCCCTA	360
CMCTTGAWTC	CNCNCCTTNN	NNTNCCNTNA	TNTGCCCGCC	CNCCTCCTNG	NGTCAACCNG	420
NATCTGCACT	ANCTCCCTCN	CCCCTTNTGG	ANTCTCNTCC	TTCAANTAAN	NTTATCCTTN	480
ACNCCCCCCT	CNCCTTTCCC	CTNCCNCCCN	TNATCCCNNG	NCCNCTATCA	NTCNTNCCCT	540
CNCTNTNCTN	CNNATCGTTC	CNCCTNNTAA	CTACNCTTTN	NACNANNCTT	CACTNATNCC	600
NGNNANTTCT	TTCTTCCCT	CCCNACGCNN	TGCGTGCGCC	CGTCTNGCCT	NNNCTNCGNA	660
CCCNNACTTT	ATTACCTTT	NCACCCTAGC	NCTCTACTTN	ACCCANCCNC	TCCTACCTCC	720
NGGNCCACCC	NNCCCTNATC	NCTNNCTCTN	TCNNCTCNTT	CCCC		764

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CAAGTGTAGG	CACAGTGATG	AAAGCCTGGA	GCAAACACAA	TCTGTGGGTA	ATTAACGTTT	60
ATTTCTCCCC	TTCCAGGAAC	GTCTTGCATG	GATGATCAAA	GATCAGCTCC	TGGTCAACAT	120
AAATAAGCTA	GTTTAAGATA	CGTTCCCTTA	CACTTGA			157

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

ATTCGATTGT	ACTCAGACAA	CAATATGCTA	AGTGGAAGAA	GTCAGTCACA	AAAGACCACA	60
TACTGTATGA	CTTCATTTAC	ATTAAGTGTC	CAGAATAGGC	AAATCCGTAG	AGACAGAAAG	120
TAGATGAGCA	GCTGCCTAGG	TCTGAGTACA				150

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATTCGATTTT TTTTTTTTTT GCCATGATGA AATTCTTACT CCCTCAGATT TTTGTCTGG	60
ATAAATGCAA GTCTCACCAC CAGATGTGAA ATTACAGTAA ACTTTGAAGG AATCTCCTGA	120
GCAACCTTGG TTAGGATCAA TCCAATATTC ACCATCTGGG AAGTCAGGAT GGCTGAGTTG	180
CAGGTCTTTA CAAGTTCGGG CTGGATTGGT CTGAGTACA	219

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATTCGATTCT TGAGGCTACC AGGAGCTAGG AGAAGAGGCA TGAACAAAT TTTCCCTCAT	60
ATCCATACTC AGAAGGAACC AACCTGCTG ACACCTTAAT TTCAGCTTCT GGCCTCTAGA	120
ACTGTGAGAG AGTACATTTC TCTTGTTTA AGCCAAGAGA ATCTGTCTTT TGGTACTTTA	180
TATCATAGCC TCAAGA	196

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

ATTCGATTTT AGTCCAGTCC CAGAACCCAC ATTGTCAATT ACTACTCTGT ARAAGATTCA	60
TTTGTTGAAA TTCATTGAGT AAAACATTTA TGATCCCTTA ATATATGCCA ATTACCATGC	120
TAGGTACTGA AGATTCAAGT GACCGAGATG CTAGCCCTTG GGTTCAGTG ATCCCTCTCC	180
CAGAGTGCAC TGGACTGAA	199

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ATTTCGATTCT	TGAGGCTACA	AACCTGTACA	GTATGTTACT	CTACTGAATA	CTGTAGGCAA	60
TAGTAATACA	GAAGCAAGTA	TCTGTATATG	TAAACATTAA	AAAGGTACAG	TGAAACTTCA	120
GTATTATAAT	CTTAGGGACC	ACCATTATAT	ATGTGGTCCA	TCATTGGCCA	AAAAAAAAAA	180
AA						182

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCAGGAGGA	GAAATGTAAT	TCCATATTTT	ATTTGAAACT	TATTCCATAT	TTTAATTGGA	60
TATTGAGTGA	TTGGGTTATC	AAACACCCAC	AAACTTTAAT	TTTGTTAAAT	TTATATGGCT	120
TTGAAATAGA	AGTATAAGTT	GCTACCATTT	TTTGATAACA	TTGAAAGATA	GTATTTTACC	180
ATCTTTAATC	ATCTTGGAAG	ATACAAGTCC	TGTGAACAAC	CACTCTTTCA	CCTAGCAGCA	240
TGAGGCCAAA	AGTAAAGGCT	TTAAATTATA	ACATATGGGA	TTCTTAGTAG	TATGTTTTTT	300
TCTTGAAACT	CAGTGGCTCT	ATCTAACCTT	ACTATCTCCT	CACTCTTTCT	CTAAGACTAA	360
ACTCTAGGCT	CTTAAAAATC	TGCCCACACC	AATCTTAGAA	GCTCTGAAAA	GAATTTGTCT	420
TTAAATATCT	TTTAATAGTA	ACATGTATTT	TATGGACCAA	ATTGACATTT	TCGACTATTT	480
TTTCCAAAAA	AGTCAGGTGA	ATTTTCAGCAC	ACTGAGTTGG	GAATTTCTTA	TCCCAGAAGA	540
CCAACCAATT	TCATATTTAT	TTAAGATTGA	TTCCATACTC	CGTTTTCAAG	GAGAATCCCT	600
GCAGTCTCCT	TAAAGGTAGA	ACAAATACTT	TCTATTTTTT	TTTCACCATT	GTGGGATTGG	660
ACTTTAAGAG	GTGACTCTAA	AAAAACAGAG	AACAAATATG	TCTCAGTTGT	ATTAAGCACG	720
GACCCATATT	ATCATATTCA	CTTAAAAAAA	TGATTTCCCTG	TGCACCTTTT	GGCAACTTCT	780
CTTTTCAATG	TAGGGAAAAA	CTTAGTCACC	CTGAAAACCC	ACAAAATAAA	TAAAACCTGT	840
AGATGTGGGC	AGAAGGTTTG	GGGGTGGACA	TTGTATGTGT	TTAAATTAAA	CCCTGTATCA	900
CTGAGAAGCT	GTGTATGGG	TCAGAGAAAA	TGAATGCTTA	GAAGCTGTTT	ACATCTTCAA	960
GAGCAGAAGC	AAACCACATG	TCTCAGCTAT	ATTATTATTT	ATTTTTTATG	CATAAAGTGA	1020
ATCATTTCTT	CTGTATTAAT	TTCCAAAGGG	TTTTACCCTC	TATTTAAATG	CTTTGAAAAA	1080
CAGTGCATTG	ACAATGGGTT	GATATTTTTT	TTTAAAAGAA	AAATATAATT	ATGAAAGCCA	1140
AGATAATCTG	AAGCCTGTTT	TATTTTAAAA	CTTTTATATG	TCTGTGGTTG	ATGTTGTTTG	1200
TTTGTGTTG	TCTATTTTGT	TGGTTTTTTT	CTTTGTTTTT	TGTTTTGTTT	TGTTTTGTTT	1260
KGCATACTAC	ATGCAGTTCT	TTAACCAATG	TCTGTTTGGC	TAATGTAATT	AAAGTTGTTA	1320
ATTTATATGA	GTGCATTTCA	ACTATGTCAA	TGGTTTCTTA	ATATTTATTG	TGTAGAAGTA	1380
CTGGTAATTT	TTTTATTTAC	AATATGTTTA	AAGAGATAAC	AGTTTGATAT	GTTTTCATGT	1440
GTTTATAGCA	GAAGTTATTT	ATTTCTATGG	CATTCCAGCG	GATATTTTGG	TGTTTGCGAG	1500
GCATGCAGTC	AATATTTTGT	ACAGTTAGTG	GACAGTATTC	AGCAACGCCT	GATAGCTTCT	1560
TTGGCCTTAT	GTAAATAAAA	AAGACCTGTT	TGGGATGTAT	TTTTTATTTT	TAAAAAAA	1620
AAAAAAAAAA	AAAAAAAAAA	AAAAAA				1646

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780
TTTGCTTGTC	CCTCTTGTTT	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTTCTGG	840
GGACTTTACC	CCACCAGGCA	GCTCTGTGGA	GCTTGTCAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CATGAAGGCG	CTGTCATCGT	AGTCTCCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCCTG	CAGCAGGGGA	AGCAGTGCCA	GCACCACTTG	CACCTCTTGC	TCCCAAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTGCCACG	TTGCTCTTGC	CGCTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATTACAAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTACT	GAAATCATGT	CATCTGCGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAT	1380
AATATAATTT	TCCTCTGGAG	CCATATGGAT	GAACATGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCCTCAGCC	ATCAGCGCCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGAT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAA	1620
TCACATAAAC	AGAATTAAAA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAA	TCCAGCATCC	TTGTATTTAT	TGTTGCAGTT	CTCAGAGGAA	ATGCTTCTAA	1740
CTTTTCCCCA	TTTAGTATTA	TGTTGGCTGT	GGGCTTGTC	TAGGTGGTTT	TTATTACTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTTGCT	GAGGGTTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780

TTTGCTTGTC	CCTCTTGTTT	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTTCTGG	840
GGACTTTTACC	CCACCAGGCA	GCTCTGTGGA	GCTTGTCCAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CATGAAGGCG	CTGTCATCGT	AGTCTCCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCCTG	CAGCAGGGGA	AGCAGTGGCA	GCACCACTTG	CACCTCTTGC	TCCCCAAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTGCCACG	TTGCTCTTGC	CGTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTCAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATTACAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTACT	GAAATCATGT	CATCTGCGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAAT	1380
AATATAATTT	TCCTCTGGAG	CCATATGGAT	GAACATGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCCTCAGCC	ATCAGCGCCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGAT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAA	1620
TCACATAAAC	AGAATTAATA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAA	TCCAGCATCC	TTGTATTTAT	TGTTGCAGTT	CTCAGAGGAA	ATGCTTCTAA	1740
CTTTTCCCCA	TTTAGTATTA	TGTTGGCTGT	GGGCTTGTC	TAGGTGGTTT	TTATTACTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTTGCT	GAGGGTTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CTTGAGCTTC	CAAATAYGGA	AGACTGGCCC	TTACACASGT	CAATGTAAAA	ATGAATGCAT	60
TTCAGTATTT	TGAAGATAAA	ATTRGTAGAT	CTATACCTTG	TTTTTTGATT	CGATATCAGC	120
ACCRATAAAG	AGCAGTGCTT	TGGCCATTAA	TTTATCTTTC	ATTRTAGACA	GCRTAGTGYA	180
GAGTGGTATT	TCCATACTCA	TCTGGAATAT	TTGGATCAGT	GCCATGTTCC	AGCAACATTA	240
ACGCACATT	ATCTTCTTGG	CATTGTACGG	CCTGTACAGT	TTAGACCCAA	AAACAAATTA	300
CATATCTTAG	GAATTCAAAA	TAACATTCCA	CAGCTTTCAC	CAACTAGTTA	TATTTAAAGG	360
AGAAAATCA	TTTTTATGCC	ATGTATTGAA	ATCAAACCCA	CCTCATGCTG	ATATAGTTGG	420
CTACTGCATA	CCTTTATCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	480
CGTCTGTCCA	GCAGGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	540
GCAGTCCTAT	GAGAGTGAGA	AGACTTTTTA	GGAAATTGTA	GTGCACTAGC	TACAGCCATA	600
GCAATGATTC	ATGTAAGTGC	AAACACTGAA	TAGCCTGCTA	TTACTCTGCC	TTCAAAAAAA	660
AAAAAAA						668

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GGGTCGCCCC	GGGGGSGCGT	GGGCTTTCCT	CGGGTGGGTG	TGGGTTTTCC	CTGGGTGGGG	60
TGGGCTGGGC	TRGAATCCCC	TGCTGGGGTT	GGCAGGTTTT	GGCTGGGATT	GACTTTTYTC	120
TTCAAACAGA	TTGGAAACCC	GGAGTTACCT	GCTAGTTGGT	GAACTGGTT	GGTAGACGCG	180

ATCTGTTGGC	TACTACTGGC	TTCTCCTGGC	TGTTAAAAGC	AGATGGTGGT	TGAGGTTGAT	240
TCCATGCCCG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTTGCTTCCC	CTGCTGCAGG	GAGAGCGGCA	AGAGCAACGT	GGGCACTTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	GGGGAGACTA	CGATGACAGT	600
GCCTTCATGG	AGCCCAGGTA	CCACGTCCGT	GGAGAAGATC	TGGACAAGCT	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGGTA	CACTGACGTG	720
AACAAGAAGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	CCTCTGCCAA	TGGGAATTCA	780
GAAGTAGTAA	AACCTSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	AAGATAAATT	AATGGCCAAA	GCACTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGGTATAGAT	CTACTAATTT	TATCTTCAAA	ATACTGAAAT	GCATTCATTT	1080
TAACATTGAC	GTGTGTAAGG	GCCAGTCTTC	CGTATTTGGA	AGCTCAAGCA	TAACCTGAAT	1140
GAAAATATTT	TGAAATGACC	TAATTATCTM	AGACTTTTATT	TTAAATATTG	TTATTTTCAA	1200
AGAAGCATT	GAGGGTACAG	TTTTTTTTTT	TTAAATGCAC	TTCTGGTAAA	TACTTTTGTT	1260
GAAAACACTG	AATTTGTAAA	AGGTAATACT	TACTATTTTT	CAATTTTTC	CTCCTAGGAT	1320
TTTTTTCCCC	TAATGAATGT	AAGATGGCAA	AATTTGCCCT	GAAATAGGTT	TTACATGAAA	1380
ACTCCAAGAA	AAGTTAAACA	TGTTTCAGTG	AATAGAGATC	CTGCTCCTTT	GGCAAGTTCC	1440
TAAAAAACAG	TAATAGATAC	GAGGTGATGC	GCCTGTCACT	GGCAAGGTTT	AAGATATTTT	1500
TGATCTCGTG	CC					1512

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGGTCGCCCA	GGGGGSGCGT	GGGCTTTCCT	CGGGTGGGTG	TGGGTTTTTC	CTGGGTGGGG	60
TGGGCTGGGC	TRGAATCCCC	TGCTGGGGTT	GGCAGGTTTT	GGCTGGGATT	GACTTTTTYTC	120
TTCAAACAGA	TTGGAAACCC	GGAGTTACCT	GCTAGTTGGT	GAAACTGGTT	GGTAGACGCG	180
ATCTGTTGGC	TACTACTGGC	TTCTCCTGGC	TGTTAAAAGC	AGATGGTGGT	TGAGGTTGAT	240
TCCATGCCCG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTTGCTTCCC	CTGCTGCAGG	GAGAGCGGCA	AGAGCAACGT	GGGCACTTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	GGGGAGACTA	CGATGACAGY	600
GCCTTCATGG	AKCCCAGGTA	CCACGTCCRT	GGAGAAGATC	TGGACAAGCT	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGGGA	CACKGAYGTG	720
AACAAGARGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	CCTCTGCCAA	TGGGAATTCA	780
GAAGTAGTAA	AACCTSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	AAGATAAATT	AATGGCCAAA	GCACTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGCATGGCCT	CACACCACTG	YTACTTGGTR	TACATGAGCA	AAAACAGCAA	1080
GTSGTGAAAT	TTTTAATYAA	GAAAAAAGCG	AATTTAAAT	GCRCTGGATA	GATATGGAAG	1140
RACTGCTCTC	ATACTTGCTG	TATGTTGTGG	ATCAGCAAGT	ATAGTCAGCC	YTCTACTTGA	1200
GCAAAATRTT	GATGTATCTT	CTCAAGATCT	GGAAAGACGG	CCAGAGAGTA	TGCTGTTTCT	1260

AGTCATCATC	ATGTAATTTG	CCAGTTACTT	TCTGACTACA	AAGAAAAACA	GATGTTAAAA	1320
ATCTCTTCTG	AAAACAGCAA	TCCAGAACAA	GACTTAAAGC	TGACATCAGA	GGAAGAGTCA	1380
CAAAGGCTTA	AAGGAAGTGA	AAACAGCCAG	CCAGAGGCAT	GGAAACTTTT	AAATTTAAAC	1440
TTTTGGTTTA	ATGTTTTTTT	TTTTTGCCTT	AATAATATTA	GATAGTCCCA	AATGAAATWA	1500
CCTATGAGAC	TAGGCTTTGA	GAATCAATAG	ATTCTTTTTT	TAAGAATCTT	TTGGCTAGGA	1560
GCGGTGTCTC	ACGCCTGTAA	TTCCAGCACC	TTGAGAGGCT	GAGGTGGGCA	GATCACGAGA	1620
TCAGGAGATC	GAGACCATCC	TGGCTAACAC	GGTGAAACCC	CATCTCTACT	AAAAATACAA	1680
AAACTTAGCT	GGGTGTGGTG	GCGGGTGCCT	GTAGTCCCAG	CTACTCAGGA	RGCTGAGGCA	1740
GGAGAATGGC	ATGAACCCGG	GAGGTGGAGG	TTGCAGTGAG	CCGAGATCCG	CCACTACACT	1800
CCAGCCTGGG	TGACAGAGCA	AGACTCTGTC	TCAAAAAAAA	AAAAAAAAAA	AAA	1853

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GGCACGAGAA	TTAAACCCT	CAGCAAAACA	GGCATAGAAG	GGACATACCT	TAAAGTAATA	60
AAAACCACCT	ATGACAAGCC	CACAGCCAAC	ATAATACTAA	ATGGGGAAAA	GTTAGAAGCA	120
TTTCCTCTGA	GAAGTCAAC	AATAAATACA	AGGATGCTGG	ATTTTGTCAA	ATGCCTTTTC	180
TGTGTCTGTT	GAGATGCTTA	TGTGACTTTG	CTTTTAATTC	TGTTTATGTG	ATTATCACAT	240
TTATTGACTT	GCCTGTGTTA	GACCGGAAGA	GCTGGGGTGT	TTCTCAGGAG	CCACCGTGTG	300
CTGCGGCAGC	TTGCGGATAA	CTTGAGGCTG	CATCACTGGG	GAAGAAACAC	AYTCCTGTCC	360
GTGGCGCTGA	TGGCTGAGGA	CAGAGCTTCA	GTGTGGCTTC	TCTGCGACTG	GCTTCTTCGG	420
GGAGTTCTTC	CTTCATAGTT	CATCCATATG	GCTCCAGAGG	AAAATTATAT	TATTTTGTTA	480
TGGATGAAGA	GTATTACGTT	GTGCAGATAT	ACTGCAGTGT	CTTCATCTCT	TGATGTGTGA	540
TTGGGTAGGT	TCCACCATGT	TGCCGCAGAT	GACATGATTT	CAGTACCTGT	GTCTGGCTGA	600
AAAGTGTTTG	TTTGTGAATG	GATATTGTGG	TTTCTGGATC	TCATCCTCTG	TGGGTGGACA	660
GCTTTCTCCA	CCTTGCTGGA	AGTGACCTGC	TGTCCAGAAG	TTTGATGGCT	GAGGAGTATA	720
CCATCGTGCA	TGCATCTTTC	ATTTCCTGCA	TTTCTTCCTC	CCTGGATGGA	CAGGGGGAGC	780
GGCAAGAGCA	ACGTGGGCAC	TTCTGGAGAC	CACAACGACT	CCTCTGTGAA	GACGCTTGGG	840
AGCAAGAGGT	GCAAGTGGTG	CTGCCACTGC	TTCCCTGCTG	GCAGGGGAGC	GGCAAGAGCA	900
ACGTGGTTCG	TTGGGGAGAC	TACGATGACA	GCGCCTTCAT	GGATCCCAGG	TACCACGTCC	960
ATGGAGAAGA	TCTGGACAAG	CTCCACAGAG	CTGCCTGGTG	GGGTAAAGTC	CCCAGAAAGG	1020
ATCTCATCGT	CATGCTCAGG	GACACGGATG	TGAACAAGAG	GGACAAGCAA	AAGAGGACTG	1080
CTCTACATCT	GGCCTCTGCC	AATGGGAATT	CAGAAGTAGT	AAAACCTCGT	CTGGACAGAC	1140
GATGTCAACT	TAATGTCCTT	GACAACAAAA	AGAGGACAGC	TCTGACAAAG	GCCGTACAAT	1200
GCCAGGAAGA	TGAATGTGCG	TTAATGTTGC	TGGAACATGG	CACTGATCCA	AATATTCCAG	1260
ATGAGTATGG	AAATACCACT	CTACACTATG	CTGTCTACAA	TGAAGATAAA	TTAATGGCCA	1320
AAGCACTGCT	CTTATACGGT	GCTGATATCG	AATCAAAAAA	CAAGCATGGC	CTCACACCAC	1380
TGCTACTTGG	TATACATGAG	CAAAAAACAGC	AAGTGGTGAA	ATTTTAAATC	AAGAAAAAAG	1440
CGAATTTAAA	TGCGCTGGAT	AGATATGGAA	GAAGTGTCTT	CATACTTGCT	GTATGTTGTG	1500
GATCAGCAAG	TATAGTCAGC	CCTCTACTTG	AGCAAAATGT	TGATGTATCT	TCTCAAGATC	1560
TGGAAAGACG	GCCAGAGAGT	ATGCTGTTTC	TAGTCATCAT	CATGTAATTT	GCCAGTTACT	1620
TTCTGACTAG	AAAGAAAAAC	AGATGTTAAA	AATCTCTTCT	GAAAACAGCA	ATCCAGAACA	1680
AGACTTAAAG	CTGACATCAG	AGGAAGAGTC	ACAAAGGCTT	AAAGGAAGTG	AAAACAGCCA	1740
GCCAGAGGCA	TGGAAACTTT	TAAATTTAAA	CTTTTGGTTT	AATGTTTTTT	TTTTTTGCCT	1800
TAATAATATT	AGATAGTCCC	AAATGAAATW	ACCTATGAGA	CTAGGCTTTG	AGAATCAATA	1860
GATTCTTTTT	TTAAGAATCT	TTTGGCTAGG	AGCGGTGTCT	CACGCCTGTA	ATTCCAGCAC	1920
CTTGAGAGGC	TGAGGTGGGC	AGATCACGAG	ATCAGGAGAT	CGAGACCATC	CTGGCTAACA	1980
CGGTGAAACC	CCATCTCTAC	TAAAAATACA	AAAACCTTAGC	TGGGTGTGGT	GGCGGGTGCC	2040

TGTAAGTCCCA	GCTACTCAGG	ARGCTGAGGC	AGGAGAATGG	CATGAACCCG	GGAGGTGGAG	2100
GTTGCAGTGA	GCCGAGATCC	GCCACTACAC	TCCAGCCTGG	GTGACAGAGC	AAGACTCTGT	2160
CTCAAAAAAA	AAAAAAAAAA	AAAA				2184

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

TGCACGCATC	GGCCAGTGTC	TGTGCCACGT	ACACTGACGC	CCCCTGAGAT	GTGCACGCCG	60
CACGCGCACG	TTGCACGCGC	GCGAGCGGCT	TGGCTGGCTT	GTAACGGCTT	GCACGCGCAC	120
GCCGCCCCCG	CATAACCGTC	AGACTGGCCT	GTAACGGCTT	GCAGGCGCAC	GCCGCGCACG	180
CGTAACGGCT	TGGCTGCCCT	GTAACGGCTT	GCACGTGCAT	GCTGCACGCG	CGTTAACGGC	240
TTGGCTGGCA	TGTAGCCGCT	TGGCTTGGCT	TTGCATTYTT	TGCTKGGCTK	GGCGTTGKTY	300
TCTTGGATTG	ACGCTTCCTC	CTTGATKGA	CGTTTCCTCC	TTGGATKGAC	GTTTCYTYTY	360
TCGCGTTTCT	TTGCTGGACT	TGACCTTTTY	TCTGCTGGGT	TTGGCATTCC	TTTGGGGTGG	420
GCTGGGTGTT	TTCTCCGGGG	GGGKTKGCCC	TTCTTGGGGT	GGGCGTGGGK	CGCCCCCAGG	480
GGGCGTGGGC	TTTCCCCGGG	TGGGTGTGGG	TTTTCTTGGG	GTGGGGTGGG	CTGTGCTGGG	540
ATCCCCCTGC	TGGGGTTGGC	AGGGATTGAC	TTTTTTCTTC	AAACAGATTG	GAAACCCGGA	600
GTAACNTGCT	AGTTGGTGAA	ACTGTTGGT	AGACGCGATC	TGCTGGTACT	ACTGTTTCTC	660
CTGGCTGTTA	AAAGCAGATG	GTGGCTGAGG	TTGATTCAAT	GCCGGCTGCT	TCTTCTGTGA	720
AGAAGCCATT	TGGTCTCAGG	AGCAAGATGG	GCAAGTGGTG	CGCCACTGCT	TCCCCTGCTG	780
CAGGGGGAGC	GGCAAGAGCA	ACGTGGGCAC	TTCTGGAGAC	CACAACGACT	CCTCTGTGAA	840
GACGCTTGGG	AGCAAGAGGT	GCAAGTGGTG	CTGCCCCACTG	CTTCCCCTGC	TGCAGGGGAG	900
CGCAAGAGC	AACGTGGKCG	CTTGGGGAGA	CTACGATGAC	AGCGCCTTCA	TGGAKCCCAG	960
GTACCACGTC	CRTGGAGAAG	ATCTGGACAA	GCTCCACAGA	GCTGCCTGGT	GGGGTAAAGT	1020
CCCCAGAAAG	GATCTCATCG	TCATGCTCAG	GGACACTGAY	GTGAACAAGA	RGGACAAGCA	1080
AAAGAGGACT	GCTCTACATC	TGGCCTCTGC	CAATGGGAAT	TCAGAAGTAG	TAAAACTCGT	1140
GCTGGACAGA	CGATGTCAAC	TTAATGTCCT	TGACAACAAA	AAGAGGACAG	CTCTGACAAA	1200
GGCCGTACAA	TGCCAGGAAG	ATGAATGTGC	GTTAATGTTG	CTGGAACATG	GCACTGATCC	1260
AAATATTCCA	GATGAGTATG	GAAATACCAC	TCTACACTAT	GCTGTCTACA	ATGAAGATAA	1320
ATTAATGGCC	AAAGCACTGC	TCTTATACGG	TGCTGATATC	GAATCAAAAA	ACAAGGTATA	1380
GATCTACTAA	TTTTATCTTC	AAAATACTGA	AATGCATTCA	TTTTAACATT	GACGTGTGTA	1440
AGGGCCAGTC	TTCCGTATTT	GGAAGCTCAA	GCATAACTTG	AATGAAAATA	TTTTGAAATG	1500
ACCTAATTAT	CTAAGACTTT	ATTTTAAATA	TTGTTATTTT	CAAAGAAGCA	TTAGAGGGTA	1560
CAGTTTTTTT	TTTTTAAATG	CACTTCTGGT	AAATACTTTT	GTTGAAAACA	CTGAATTTGT	1620
AAAAGGTAAT	ACTTACTATT	TTTCAATTTT	TCCCTCCTAG	GATTTTTTTC	CCCTAATGAA	1680
TGTAAGATGG	CAAAATTTGC	CCTGAAATAG	GTTTTACATG	AAAACCTCAA	GAAAAGTTAA	1740
ACATGTTTCA	GTGAATAGAG	ATCCTGCTCC	TTTGGCAAGT	TCCTAAAAAA	CAGTAATAGA	1800
TACGAGGTGA	TGCGCCTGTC	AGTGGCAAGG	TTTAAGATAT	TTCTGATCTC	GTGCC	1855

CLAIMS

1. An isolated DNA molecule, comprising:
 - (a) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297;
 - (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or
 - (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.
2. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by a nucleotide sequence that:
 - (a) hybridizes to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and
 - (b) is at least 80% identical to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

3. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by:
 - (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or
 - (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained.
4. An isolated DNA or RNA molecule comprising a nucleotide sequence complementary to a DNA molecule according to any one of claims 1-3.
5. A recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.
6. A host cell transformed or transfected with an expression vector according to claim 5.
7. A polypeptide comprising an amino acid sequence encoded by a DNA molecule according to any one of claims 1-3.
8. A polypeptide according to claim 7 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.
9. A monoclonal antibody that binds to a polypeptide according to claim 7.

10. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

11. A method for determining the presence of breast cancer in a patient comprising detecting within a biological sample, at least one polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

12. The method of claims 10 or 11 wherein the biological sample is a portion of a breast tumor.

13. The method of claim 10 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody according to claim 9.

14. The method of claim 11 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

15. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, an RNA molecule encoding at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

16. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

17. The method of claims 15 or 16 wherein the biological sample is a portion of a breast tumor.

18. The method of claim 15 wherein the step of detecting comprises:

(a) preparing cDNA from RNA molecules within the biological sample;
and

(b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

19. The method of claim 16 wherein the step of detecting comprises:

(a) preparing cDNA from RNA molecules within the biological sample;
and

(b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

20. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, in a biological sample, of at least one polypeptide according to claim 7 at a first point in time;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

21. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting in a biological sample an amount of at least one polypeptide at a first point in time, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

22. The method of claims 20 or 21 wherein the biological sample is a portion of a breast tumor.

23. The method of claim 20 wherein the step of detecting comprises contacting a portion of the biological sample with a monoclonal antibody according to claim 9.

24. The method of claim 21 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252,

256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

25. The method of claim 20 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

26. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, within a biological sample, of at least one RNA molecule encoding a polypeptide according to claim 7 at a first point in time;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

27. The method of claim 26 wherein the step of detecting comprises:

- (a) preparing cDNA from RNA molecules within the biological sample; and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7.

28. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, within a biological sample, of at least one RNA molecule at a first point in time, the RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270;

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;

- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

29. A pharmaceutical composition, comprising a polypeptide according to claim 7 and a physiologically acceptable carrier.

30. A pharmaceutical composition for inhibiting the development of breast cancer, comprising a polypeptide and a physiologically acceptable carrier, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

31. A vaccine, comprising a polypeptide according to claim 7 and an immune response enhancer.

32. A vaccine, comprising a DNA molecule according to any one of claims 1-3.

33. A vaccine, comprising a recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.

34. A vaccine for inhibiting the development of breast cancer, comprising a polypeptide and an immune response enhancer, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

35. A pharmaceutical composition according to either of claims 29 or 30, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient, comprising administering to a patient.

36. A vaccine according to any one of claims 31-34, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient.

37. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies according to claim 9; and
- (b) a detection reagent.

38. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290; and
- (b) a detection reagent.

39. The kit of any one of claims 37 or 38 wherein the monoclonal antibody(s) are immobilized on a solid support.

40. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule according to claim 4.

41. The kit of claim 40, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule according to claim 4.

42. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

43. The kit of claim 42, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe containing at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

45. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe comprising at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

46. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA molecule according to claim 4.

47. The kit of claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

48. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145,

153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

49. The kit of claim 48, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

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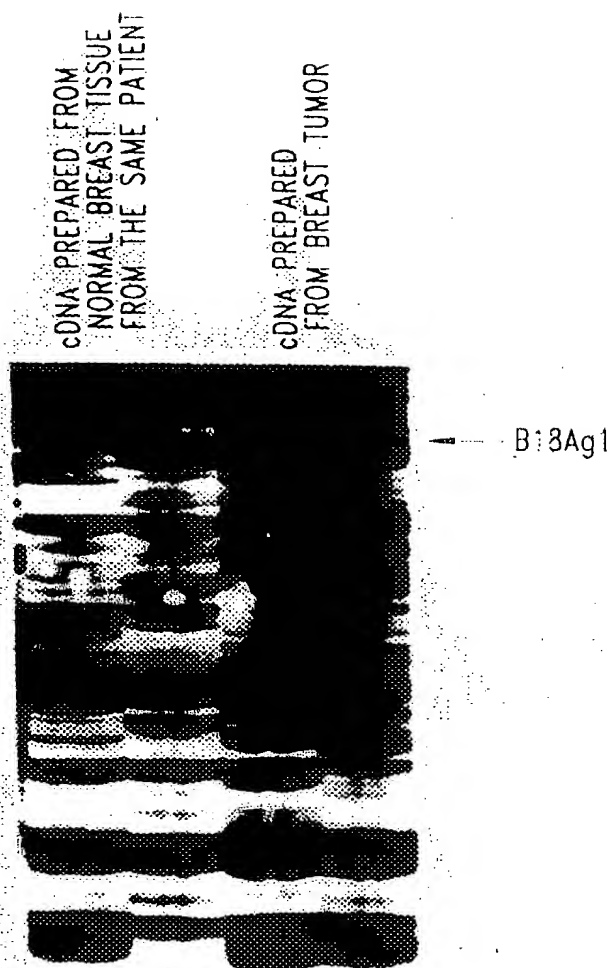


Fig. 1

SUBSTITUTE SHEET (RULE 26)

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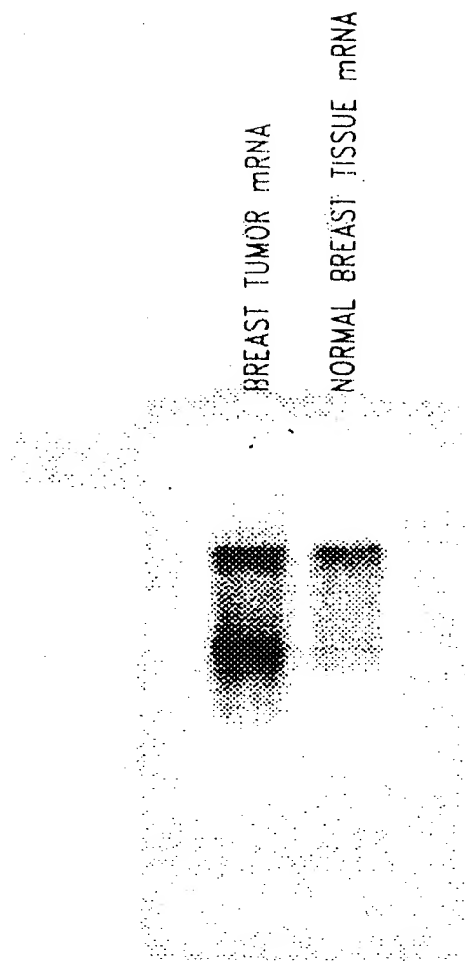
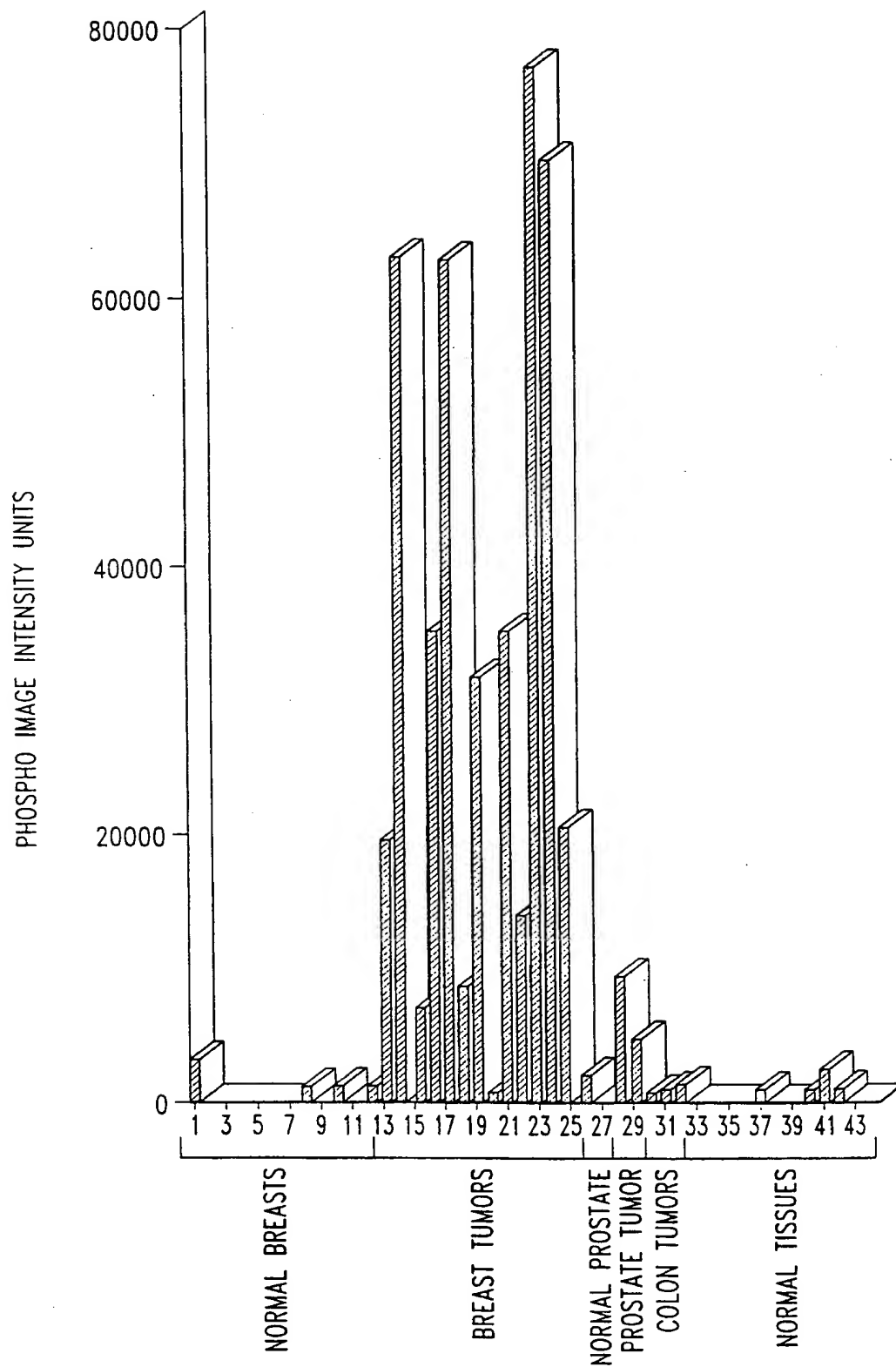


Fig. 2

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*Fig. 3*

SUBSTITUTE SHEET (RULE 26)

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GENOMIC CLONE MAP

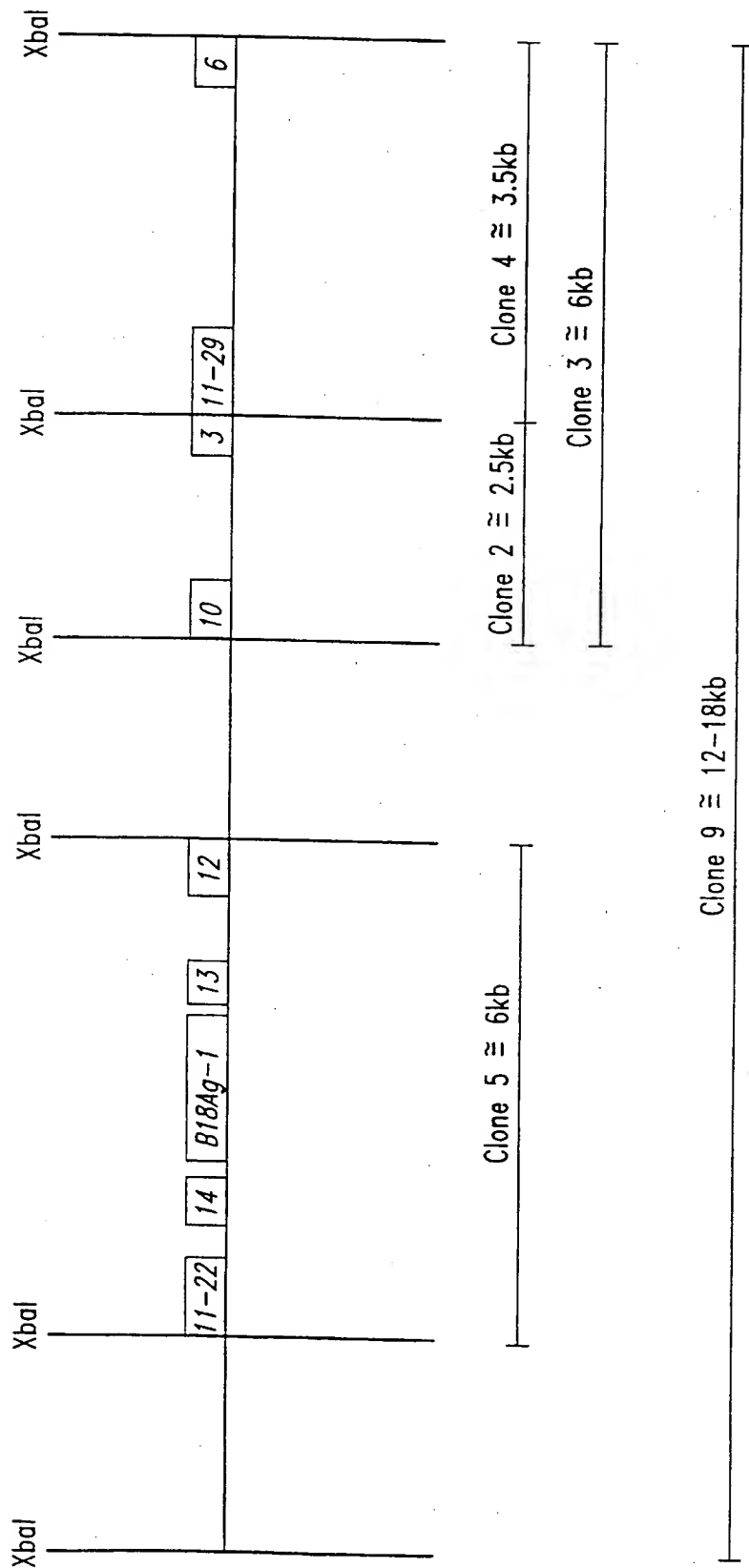


Fig. 4

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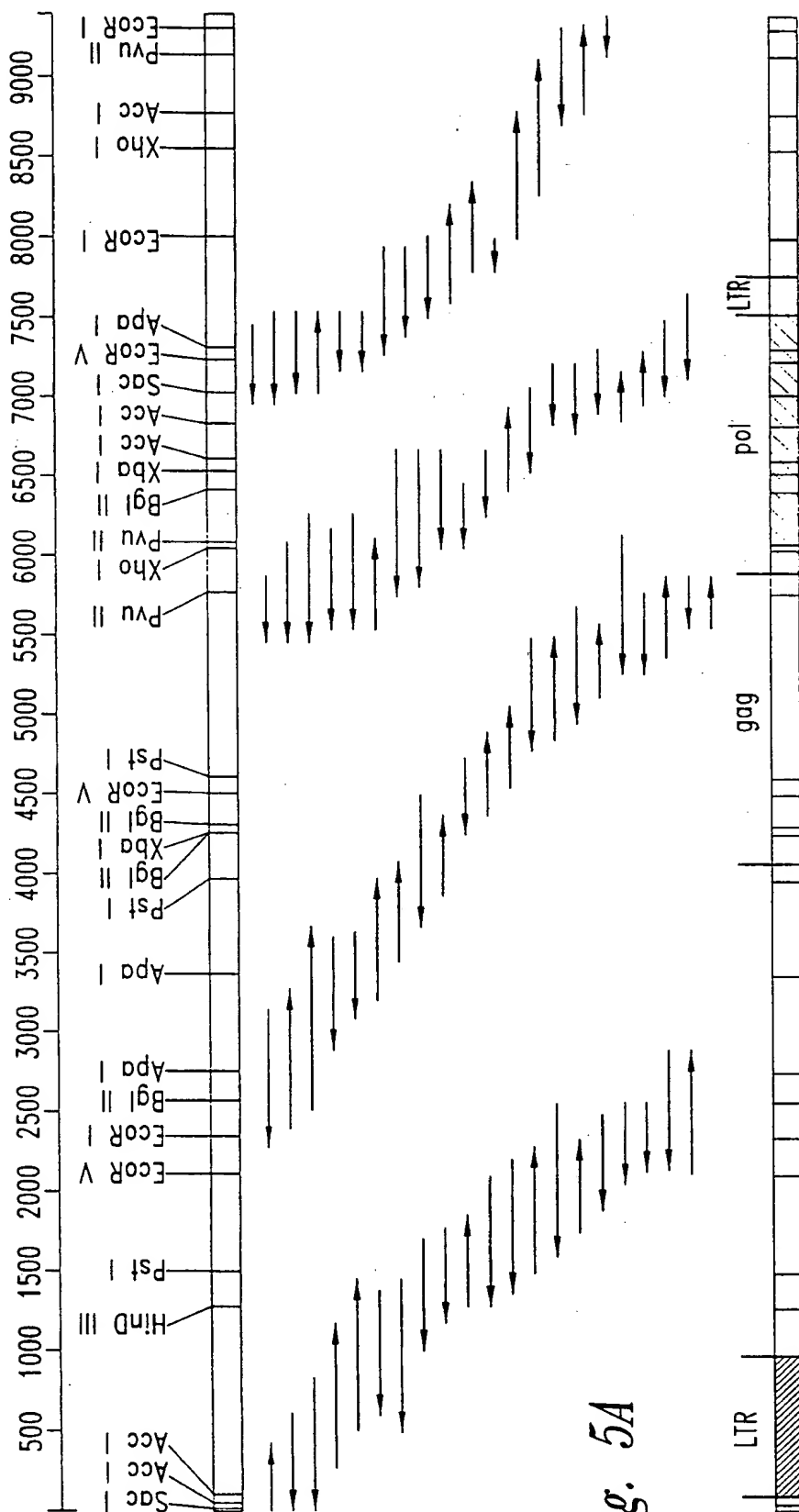


Fig. 5A

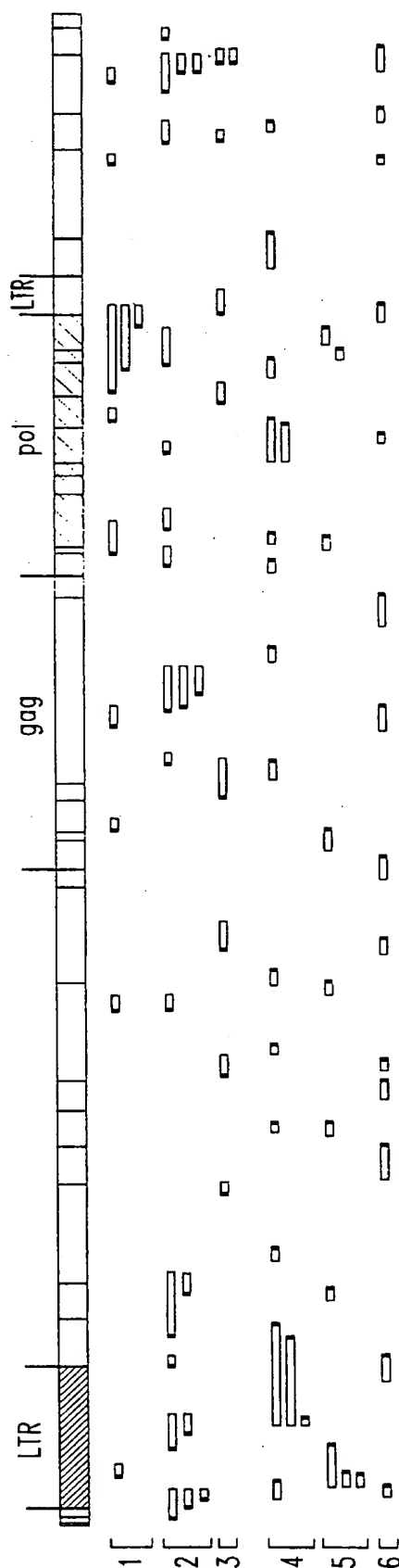


Fig. 5B

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B18Ag1

TTA	GAG	ACC	CAA	TTG	GGA	CCT	AAT	TGG	GAC	CCA	AAT	TTC	TCA	AGT	GGA	48
Leu	Glu	Thr	Gln	Leu	Gly	Pro	Asn	Trp	Asp	Pro	Asn	Phe	Ser	Ser	Gly	
1				5					10					15		
GGG	AGA	ACT	TTT	GAC	GAT	TTC	CAC	CGG	TAT	CTC	CTC	GTG	GGT	ATT	CAG	96
Gly	Arg	Thr	Phe	Asp	Asp	Phe	His	Arg	Tyr	Leu	Leu	Val	Gly	Ile	Gln	
			20					25					30			
GGA	GCT	GCC	CAG	AAA	CCT	ATA	AAC	TTG	TCT	AAG	GCG	ATT	GAA	GTC	GTC	144
Gly	Ala	Ala	Gln	Lys	Pro	Ile	Asn	Leu	Ser	Lys	Ala	Ile	Glu	Val	Val	
		35					40					45				
CAG	GGG	CAT	GAT	GAG	TCA	CCA	GGA	GTG	TTT	TTA	GAG	CAC	CTC	CAG	GAG	192
Gln	Gly	His	Asp	Glu	Ser	Pro	Gly	Val	Phe	Leu	Glu	His	Leu	Gln	Glu	
	50					55					60					
GCT	TAT	CGG	ATT	TAC	ACC	CCT	TTT	GAC	CTG	GCA	GCC	CCC	GAA	AAT	AGC	240
Ala	Tyr	Arg	Ile	Tyr	Thr	Pro	Phe	Asp	Leu	Ala	Ala	Pro	Glu	Asn	Ser	
65					70					75					80	
CAT	GCT	CTT	AAT	TTG	GCA	TTT	GTG	GCT	CAG	GCA	GCC	CCA	GAT	AGT	AAA	288
His	Ala	Leu	Asn	Leu	Ala	Phe	Val	Ala	Gln	Ala	Ala	Pro	Asp	Ser	Lys	
				85					90					95		
AGG	AAA	CTC	CAA	AAA	CTA	GAG	GGA	TTT	TGC	TGG	AAT	GAA	TAC	CAG	TCA	336
Arg	Lys	Leu	Gln	Lys	Leu	Glu	Gly	Phe	Cys	Trp	Asn	Glu	Tyr	Gln	Ser	
			100					105					110			
GCT	TTT	AGA	GAT	AGC	CTA	AAA	GGT	TTT								363
Ala	Phe	Arg	Asp	Ser	Leu	Lys	Gly	Phe								
		115					120									

Fig. 6

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCTAT	120
AA AAATAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
CT AGGAGA	196

Fig. 7

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC TTGGGGGCTC TGACTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAC TG	60
AC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
AT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCTCAGC CTGGGATTAA	240
CA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
TT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCCAGTCC CAAGCTCACT	360
CT CCTTTATAGC CTAGGAGA	388

Fig. 8

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC CTATAATCAT GTTTCATCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
AA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCAG ATAATTGATC	120
TG ATTTCTACAT CAGATGCTCT TTCCTTTCCT GTTTATTTCC TTTTATTTTC	180
GG TCGAATGTAA TAGCTTTGTT TCAAGAGAGA GTTTTGGCAG TTTCTGTAGC	240
CT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
CT ATTTTTTCCA TATTTGGGCA ACTACTA	337

Fig. 9

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1b

GC CATACAGTGC CTTTCCATTT ATTTAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTTT ACACTCCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTTCTT TCCTGGCAGC TTTTAACATT	240
TT TGTGTCTGGG GGACTGCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
CC AAGAAAAAAA AATTTTTTTG TTTTATTTGA AACTGGACCG GATAAACGGT	360
CG GCTGCTGTAT ATAGTTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
GG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTTNT	480
NA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
TC TCTTAGAGGG GGGAACTNCT A	571

Fig. 10

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACTTAAA TATATTTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAAACCAA AGTATCATAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCTTC	180
GG TGC GTGCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTTGG AGATGGAGTC	240
CA GCCCAGGGGT GGAGTACAAT GGCACAACCT CAGCTCACTG NAACCTCCGC	300
TT CATGAGATTC TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
TG CCTGGNTAAT CTTTTTTNGT TTTNGGGTAG AGATGGGGGT TTTACATGTT	420
TG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
TA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
	548

Fig. 11

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
AG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTTAGC GATAGACCAA	120
GC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTTT AAAGGGAATC CATTAAATTCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTTAT TAGCCTTACA	360
TT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATT A CCTGATGGGC	420
GA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCATCC NCAGTAAATT	480
AC AAAATATAAC TCGATTGCAT TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTTTCT TTTAGGGTTT	600
CT ACTTTACGGA TATTGGAGCA TAACGGGA	638

Fig. 12

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3c

```
ACTGATGGAT GTCGCCGGAG GCGAGGGGCC TTATCTGATG CTCGGCTGCC TGTTCTGAT   60
GTGCGCGGCG ATTGGGCTGT TTATCTCAA CACCGCCACG GCGGTGCTGA TGGCGCCTAT  120
TGCCTTAGCG GCGGCGAAGT CAATGGGCGT CTCACCCTAT CCTTTTGCCA TGGTGGTGGC  180
GATGGCGGCT TCGGCGGCGT TTATGACCCC GGTCTCCTCG CCGGTTAACA CCCTGGTGCT  240
TGGCCCTGGC AAGTACTCAT TTAGCGATTT TGTCAAATA GCGGTG                        286
```

Fig. 13

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG1

AG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
CA TTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
AC ATAAGTGCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACCTCCT	180
AA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTTGTTC TTTNCTATTN	240
CA CCTATGACCG AA	262

Fig. 14

15/22

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTTCGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
TA AATGGTGGCA GGATTTTAT TATAACATG TACCCATGCA AATTCCTAT	120
GA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTTT TAAAAGCCTA	180
AG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
TG CCTATGACCG A	261

Fig. 15

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 16

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 17

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 18

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3

AG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCCTG GCCTACGACT	60
CT GTCGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCCTCCG	120
TC NCCGTCCAGG AGGAGGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
TC ATGGTCNACA TCCC	204

Fig. 19

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B4CA1

TC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
TG ATAGTTGCTG AGTTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
CC AATCGCATGG ACATGTTAGA CTTATTTTCT GTTAATGATT NCTATTTTTA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

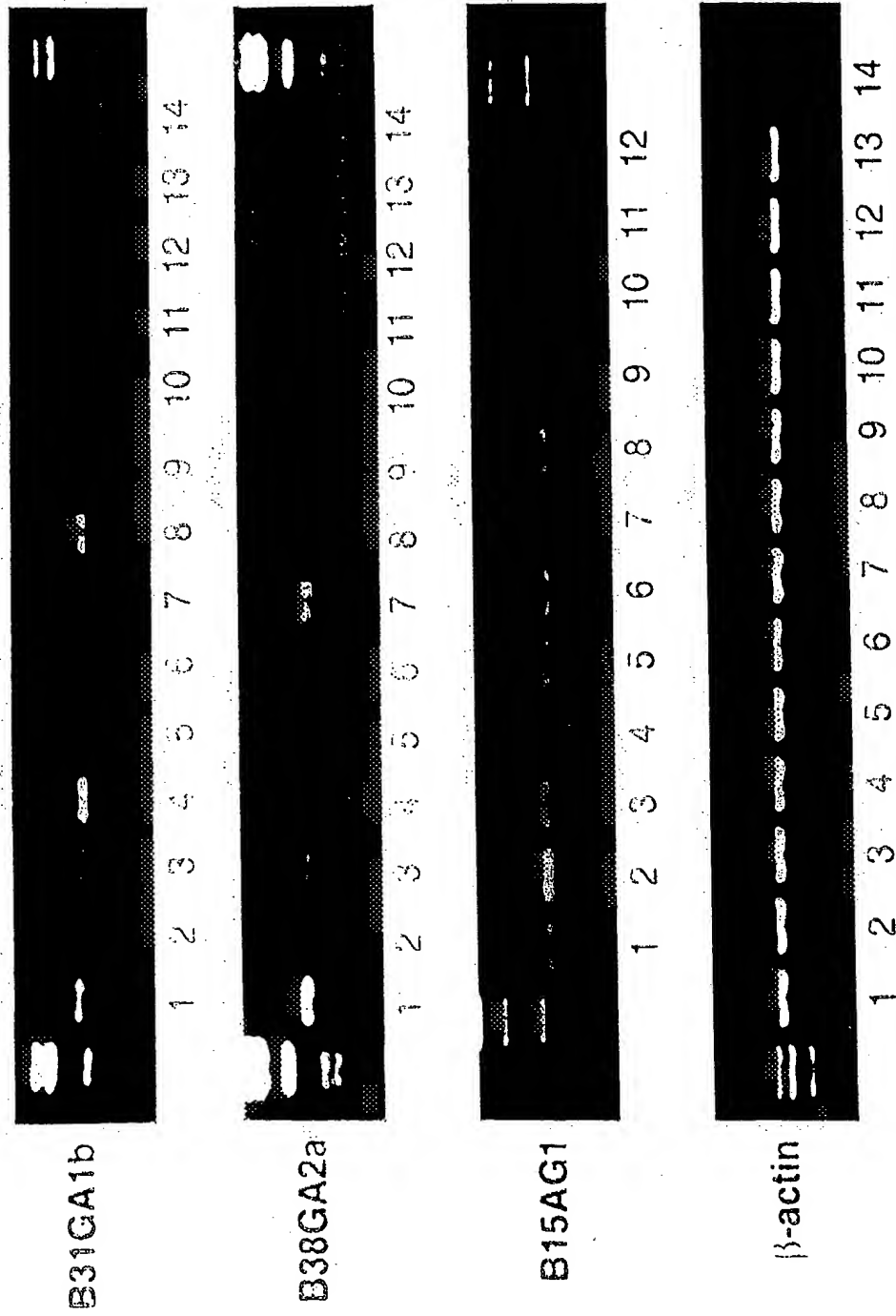


Fig. 21A

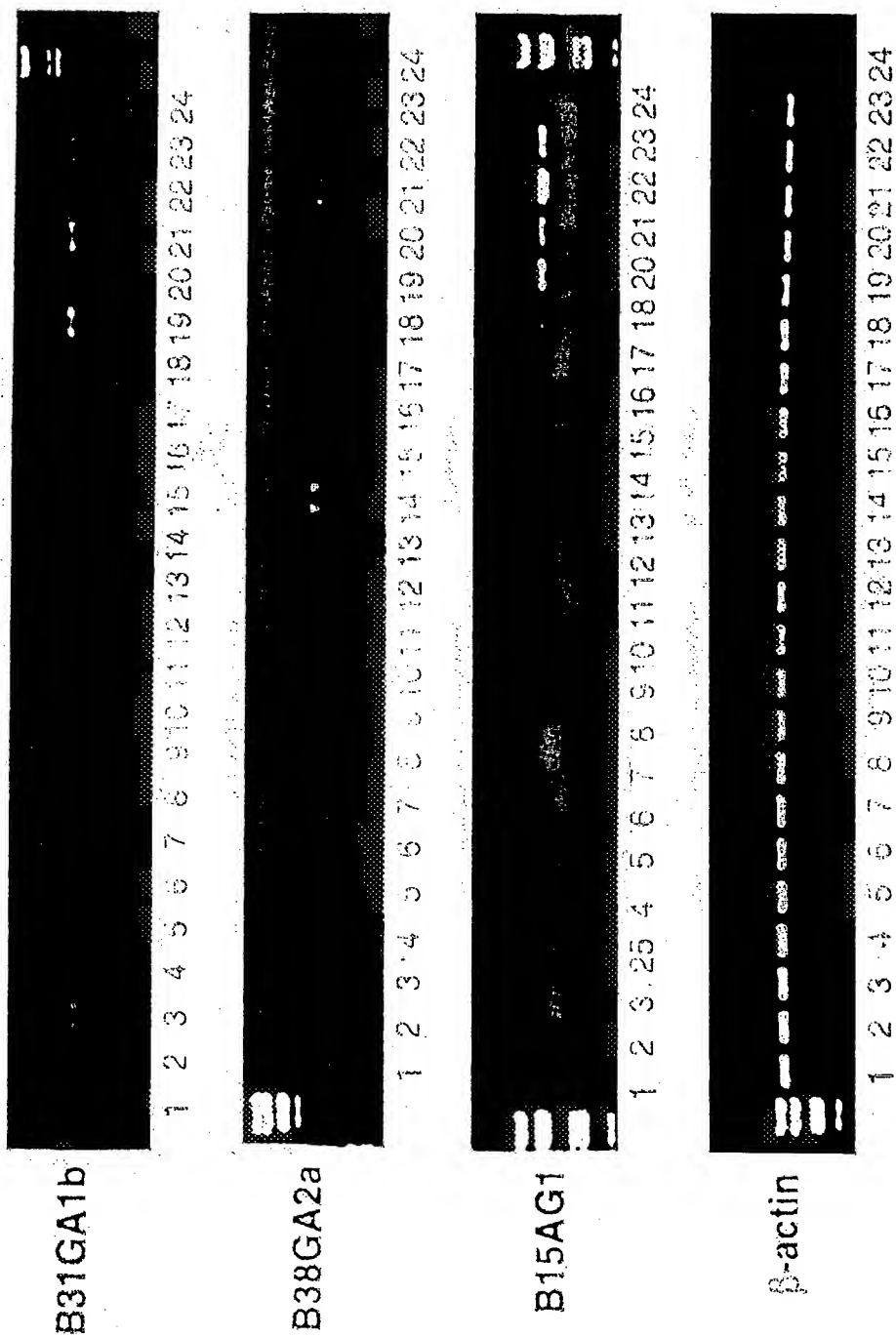


Fig. 21B



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/47, 14/82, 14/15, C12Q 1/68, G01N 33/574, A61K 38/17, 39/00	A3	(11) International Publication Number: WO 98/45328 (43) International Publication Date: 15 October 1998 (15.10.98)
(21) International Application Number: PCT/US98/06939 (22) International Filing Date: 9 April 1998 (09.04.98) (30) Priority Data: 08/838,762 9 April 1997 (09.04.97) US 08/991,789 11 December 1997 (11.12.97) US (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: FRUDAKIS, Tony, N.; P.O. Box 99232, Seattle, WA 99232-0232 (US). SMITH, John, M.; 208 - 116th Place Southeast, Everett, WA 98208 (US). REED, Steven, G.; 2843 - 122nd Place N.E., Bellevue, WA 98005 (US). (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 22 April 1999 (22.04.99)
(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER (57) Abstract <p>Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.</p>		

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/06939

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C07K14/47 C07K14/82 C07K14/15 C12Q1/68 G01N33/574
 A61K38/17 A61K39/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>WERNER T ET AL: "S71 IS A PHYLOGENETICALLY DISTINCT HUMAN ENDOGENOUS RETROVIRAL ELEMENT WITH STRUCTURAL AND SEQUENCE HOMOLOGY TO SIMIAN SARCOMA VIRUS (SSV)" VIROLOGY, vol. 174, no. 1, January 1990, pages 225-238, XP000670325</p> <p>see the whole document --- -/--</p>	<p>1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47</p>

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

31 August 1998

Date of mailing of the international search report

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Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
 NL - 2280 HV Rijswijk
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
 Fax: (+31-70) 340-3016

Authorized officer

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/06939

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 95 32311 A (CALYPTE INC) 30 November 1995 see the whole document	1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47
A	--- LEIB-MOESCH C ET AL: "EVOLUTION AND BIOLOGICAL SIGNIFICANCE OF HUMAN RETROELEMENTS" VIRUS GENES, vol. 11, no. 2/03, 1996, pages 133-145, XP000673508	
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A	--- WATSON M A ET AL: "ISOLATION OF DIFFERENTIALLY EXPRESSED SEQUENCE TAGS FROM HUMAN BREAST CANCER" CANCER RESEARCH, vol. 54, no. 17, 1 September 1994, pages 4598-4602, XP000576043 see the whole document	
A	--- BYRNE J A ET AL: "A SCREENING METHOD TO IDENTIFY GENE COMMONLY OVEREXPRESSED IN CARCINOMAS AND THE IDENTIFICATION OF A NOVEL COMPLEMENTARY DNA SEQUENCE" CANCER RESEARCH, vol. 55, no. 13, 1 July 1995, pages 2896-2903, XP002025781 see the whole document	
A	--- WO 95 19369 A (UNIV VANDERBILT) 20 July 1995 see the whole document	
A	--- WO 91 02062 A (TRITON BIOSCIENCES INC) 21 February 1991 see the whole document --- -/--	

INTERNATIONAL SEARCH REPORT

Internatl Application No

PCT/US 98/06939

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>ZEHAN CHEN ET AL: "DIFFERENTIAL EXPRESSION OF HUMAN TISSUE FACTOR IN NORMAL MAMMARY EPITHELIAL CELLS AND IN CARCINOMAS" MOLECULAR MEDICINE, vol. 1, no. 2, January 1995, pages 153-160, XP000607858 see the whole document ---</p>	
A	<p>WO 96 38463 A (UNIV WASHINGTON ;WATSON MARK A (US); FLEMING TIMOTHY P (US)) 5 December 1996 see the whole document ---</p>	
P,X	<p>WO 97 25431 A (CORIXA CORP) 17 July 1997 see the whole document ---</p>	<p>1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47</p>
P,X	<p>WO 97 25426 A (CORIXA CORP) 17 July 1997 see the whole document -----</p>	<p>1,2, 4-10,12, 13,15, 17,18, 20,22, 23, 25-27, 29, 31-33, 35-37, 39-41, 44,46,47</p>

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 06939

B x I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

B x II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see FURTHER INFORMATION sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see FURTHER INFORMATION sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33,
35-37,39-41,44,46,47 (all partially)

Invention 1:

Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 1, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to seq. ID 1, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 1, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

2. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33,
35-37,39-41,44,46,47 (all partially)

Invention 2-75:

Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 3, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 3, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 3, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences 4-26, 28-77

3. Claims: 3 (completely), 4-10,12,13,15,17,18,20,22,23,25-27,
29,31-33,35-37,39-41,44,46,47 (all partially)

Invention 76:

Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 141, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 141, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 141, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

4. Claims: 1,2,4-10,12,13,15,17,18,20,22,23,25-27,29,31-33,
35-37,39-41,44,46,47 (all partially)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 77-200:

Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 142, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 142, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 142, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences

143,146-152,154-166,168-176,178-192,194-198,200-204,206,207,209-214,216,218,219,221-240,243-245,247,250,251,253,255,257-266,268,269,271-273,275,276,278,280,281,284,288 and 291-297

5. Claims: 11,12,14,16,17,19,21,22,24,30,34,35,36,38,39,42,43,45,48,49 (all partially)

Invention 201-241:

Isolated DNA molecule comprising a nucleotide sequence with Seq.ID 78, the corresponding polypeptide, an isolated DNA or RNA molecule comprising a nucleotide sequence complementary to Seq. ID 78, a recombinant expression vector comprising that molecule, a host cell transfected with that vector, a monoclonal antibody binding to the polypeptide encoded by Seq. ID 78, as well as pharmaceutical compositions, vaccines, diagnostic methods used in the diagnosis and therapy of breast cancer.

...ibidem for each of sequences

78-86,144,145,153,167,177,193,199,205,208,215,217,220,241,242,246,248,249,252,256,267,270,274,277,279,282,283,285-287,289,290

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/06939

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